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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
No.
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
    PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       June 13, 2001, 14:23:10 ; Search time 87.97 Seconds (without alignments)
15.624 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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98
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S26798
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   Description
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| 95 | 95 | 95 | 95 | 95 | 95 | 95 | 95 | 95 | 97 | 97 | 98 | 98 | 98 | 98 | 98 |
| 96.9 | 96.9 | 96.9 | 96.9 | 96.9 | 96.9 | 96.9 | 96.9 | 96.9 | 99.0 | 99.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| 117 | 116 | 115 | 113 | 100 | 98 | 98 | 97 | 82 | 127 | 116 | 191 | 147 | 143 | 140 | 139 |
| سا | <u>-</u> - | _ | 2 | N | N | 2 | N | Ŋ | Ŋ | Ŋ | N | N | N | N | 2 |
| нзни26 | A1HUTU | H3HUTL | S25571 | PL0122 | S54856 | S26889 | S26886 | C34964 | PT0369 | B28966 | JL0048 | 137780 | S23624 | S22657 | 137781 |
| Ig heavy chain pre | • | Ig heavy chains V- | Ig heavy chain V r | Ig heavy chain V-I | Ig heavy chain V r | • | Ig heavy chain V r | Ig heavy chain pre | Ig gamma chain pre | Ig heavy chain pre | Ig heavy chain V r | Ig variable region | Ig heavy chain V r | Ig heavy chain pre | Ig variable region |

Ig heavy chain V region (DP-48) - human (fragment) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

ALIGNMENTS

S26890 RESULT

C;Accession: \$26890
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: \$26885; MUID:93021117
A;Recession: \$26890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: preliminary
A;Residues: 1-97 <TOM>
A;Residues: 1-97 <TOM>
A;Cross-references: EMBL:212348; NID:932916; PIDN:CAA78218.1; PID:932917
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM> Query Match Best Local S Matches 20 Local Similarity 100 les 20; Conservative 100.0%; Score 98; DB 2; Pred. No. 7.8e-08; ; Mismatches 0; Length 97;

В Ş N 0; Indels 0; Gaps

0;

Ig heavy chain V region (YAC-5) - human
C:Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: \$46462
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.;
Nature Genet. 7, 162-168, 1994
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the te
A;Reference number: \$46460; MUID:95004581
A;Accession: \$46462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <COO>
A;Cross-references: EMBL:227504; NID:9505430; PIDN:CAA81824.1; PID:9505431
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMMN> RESULT S46462

Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative 0; Score 98; DB 2; Pred. No. 7.8e-08; ; Mismatches 0; Length 97; Indels 0 Gaps 0

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Query Match
Best Local Similarity
Thes 20; Conserv
                                                                                                                                                                                                                                                                   A; Molecule type: DNA A; Residues: 1-98 <TOM>
A; Residues: 1-98 <TOM>
A; Cross-references: EMBL: 212354; NID: 932930; PIDN: CAA78224.1; PID: 932931
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <TMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Bird, J; Galili, N; Link, M.; Stites, D.; Sklar, J.

LEXP. Med. 168, 229-245, 1988

A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A;Reference number: PL0116; MUID:88286083

A;Reference number: PL0116; MUID:88286083

A;Reference number: PL0116; MUID:88286083

A;Residues: 1-98 (BIR)

A;Residues: 1-
                                               S
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C:Species: Homo sapiens (man)
C:Datc: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0123; S26897
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A; Residues: 1-98 <BIR>
A; Residues: 1-98 <BIR>
A; Residues: 1-98 <BIR>
A; Experimental source: B cells from patient TD with acute lymphoblastic leukemia, AL
A; Note: the sequence shows the V region (TD-VP) from one of five DNA rearrangements
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superds: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMN>
F; 11-35/Region: complementarity-determining 1
F; 49-65/Region: complementarity-determining 2
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A;Accession: PL0121
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C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
C;Accession: PL0121
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Matches 20
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s: Homo sapiens (man)
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Similarity 100.0%;
20; Conservative 0;
                                                                                              100.0%; Score 98; DB 2; larity 100.0%; Pred. No. 7.9e-08; Conservative 0; Mismatches 0;
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A; Status: preliminary A: Molecule type: DNA
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C;Accession: S26932

R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. J. Mol. Biol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885; MUID:93021117

A;Accession: S26932
                                                                                                                               Ig heavy chain V region (DP-39) - human (fragment) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross references: EMBL:Z17392; NID:g32840; PIDN:CAA78996.1; P:C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (COS 6) - human (fragment)
C:Sepecies: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29545
R:Fomilinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29543
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A; Residues: 1-98 < TOM>
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A; Molecule type: DNA
A; Residues: 1-98 < TONA
A; Cross-references: EMBL: 212353
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < TMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: $26896
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Accession: $26896
A;Accession: $26885; MUID:93021117
A;Accession: $26886
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Best Local Similarity
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Matches 20; Conserv
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Pred. No. 7.9e-08;
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Wed

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Ig heavy chain V region (DP-51) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 *sequence_revision 10-Nov-1995 *text_change 23-Jul-1999
C;Accession: $26894
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty A;Reference number: $26885; MUID:93021117
A;Accession: $26894
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C;Species: Homo saplens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26891
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Accession: S26891
A;Accession: S26891
A;Accession: S26891
A;Accession: S26891
A;Status: preliminary
A;Status: preliminary
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A; Ross-references: EMBL:212339; NID:g32898; PIDN:CAA78209.1; PID:g32899
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                  A;Cross-references: EMBL:Z12351; NID:g32924; PIDN:CAA78221.1; C;Superfamily: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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A; Residues: 1-98 < TOM>
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Similarity 100.0%;
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0; Mismatches
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hes 0;
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Ig heavy chain V region (DP-29) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S26925
R; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fifty A; Reference number: S26885; MUID:93021117
A; Accession: S26925
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A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12359; NID:g32937; PIDN:CAA78229.1; PID:g32938
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;15-98/Domain: immunoglobulin homology <IMM>
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J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups
A;Reference number: S26885; MUID:93021117
A;Reference number: S26885; MUID:93021117
A;Recession: S26933
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A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885, MUID:93021117
A;Accession: S26934
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26934
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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A; Status: preliminary
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Pred. No. 7.9
D; Mismatches
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Pred. No. 7.9e-08;
); Mismatches 0;
                                                                                  V(H) sequences reveals about fifty groups
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A:Cross references: EMBL:Z18822
C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: S36380
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J
EMBO J. 12, 725-734, 1993
                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-114 <GRIDARIA
                                                                                                                                                                                                                                                                                                         A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448
A;Accession: S36280
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117
A;Accession: S26926
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A:Molecule type: DNA
A:Residues: 1-100 <TOM>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov.1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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Pred. No. 9.2e-08;
Mismatches 0;
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Pred. No. 8.1e-08;
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hes 0;
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Search completed: June 13, 2001, 14:23:11 Job time: 742 sec

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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S60299; S1702; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5
A;Reference number: S60295; MUID:93122853
A;Accession: S60299
                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X62128; NID:g38340; PIDN:CAA44059.1; PID:g38341 A;Note: the authors did not translate the codons for residues 6, 52, 54, C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
S17079
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A; Residues: 1-117 <KU2>
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                                                                          Query Match
Best Local S
Matches 20
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Species: Homo sapiens (man)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprininae; Carassius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=88144476; PubMed=3125551; Wilson M.R., Middleton D., Warr G.W.; "Immunoglobulin heavy chain variable region and family relationships of two genes and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
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15-JUL-1999 (Rel. 38, Last annotation update)
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Immunochemistry 13:995-999(1976).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE WALDENSTROM
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                                                                                                                                              "Variable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup: definitive identification of four heavy chain hypervariable regions.";

Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGAI MYELOMA
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IG HEAVY CHAIN V-III REGION TUR.
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Сарга J.D., Кеђое J.M.;
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P01779;
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Wang A.-C., Wang I.Y., Fudenberg H.H.;
Wang A.-C., Wang I.Y., Fudenberg H.H.;
"Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977)
-i- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL GAMMOPACHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
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SEQUENCE.
Sequences of five human immunoglobulin of the VH3 subgroup: definitive identification of four h hypervariable regions.";
Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
--- MTSCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A02047; H3H026.
InterPro; IPR003006; -
Pfam; PF00047; 1g; 1.
Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                   HV30_HUMAN
P01776;
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P01764;
                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V-III REGION WAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matthysens G., Rabbitts T.H.; "Structure and multiplicity of genes for the human heavy chain variable region."; proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE
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HSSP; P01772; 2IG2.
InterPro; IPR003006; -.
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                                                  Homo sapiens (Human)
Eukaryota; Metazoa; C
                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION BUT.
                                                                                                                                                                                           HV3F_HUMAN P01767;
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Proc. Natl. Acad. Sci. U.S.A.
-!- MISCELLANEOUS: THIS CHAIN
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"Structure of antibodies with shared of the heavy chain variable regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
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IG HEAVY CHAIN V-III REGION POM.
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HSSP; P01772; 2IG2.
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Primates;
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TO DEAMIDATION

Indels

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Gaps

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RESULT 11
HV20_MOUSE
ID HV20_MOUSE
AC P01789;
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Best Local S
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Pfam; PP00047; 19; 1.
Immunoglobulin v region.
NON_TER 17 117
SEQUENCE 117 AA; 12975 M
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Best Local Similarity 90.0
Matches 18; Conservative
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MEDLINE-80049769; PubMed-115869;

Robinson E.A., Appella E.;

"Amino acid sequence of a mouse myeloma immunoglobin heavy chain (MOPC 47 A) with a 100-residue deletion.";

-1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE, LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A LIGHT-HEAVY CHAIN DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                             _MOUSE __MOUSE STANDARD; PRT; 117 AA. HV17_MOUSE STANDARD; PRT; 117 AA. P01786; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) MIS MUSEON MOPC 47A. MUSEON MOPC 47A. MUSEON MOPC 47A. Bus musculus (Mouse). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Musmaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                               LIGHT-HEAVY CHAIN DISULFIDE PIR; A02069; A1MS47. HSSP; P01789; 2MCP.
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Pfam; PF00047; 1g; 1
Immunoglobulin V region
NON_TER 115 115
SEQUENCE 115 AA; 12379
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                                                                                  1 EVQLVESGGGLVQPGGSLRL 20
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-1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) AL REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
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Torano A., Putnam F.W.;
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19; Conserv
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                    STANDARD;
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95.0%;
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PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "The three-dimensional structure of a phosphorylcholine-binding mouse immunoglobulin Fab and the nature of the antigen binding site.";

Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).

1- MISCELLANDOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                      Local
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MEDLINE-75065510; PubMed-4530984;
Segal D.M., Padlan E.A., Cohen G.H., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davies D.R.;
"The three-dimensional immunoglobulin Fab and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-80199926; PubMed=6769593;
Early P., Huang H., Davis M., Calame K., Hood L
"An immunoglobulin heavy chain variable region
three segments of DNN: VH, D and JH.";
Cell 19:981-992(1980).
                                                                                                                                                                                                                                                                                                                                                                              mmunoglobulin
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MEDLINE-75017346; PubMed-4213527;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION M603.
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2MCP; 15-JUL-92.
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H-BOND WITH THE PHOSPHATE GROUP OF PHOSPHONYLCHOLINE.
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Eukaryota; Metazoa; Chu
Mammalla; Eutherla; Ro
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MIS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE (TEPC 15).

MEDLINE-7622762; PubMed-819932;

Rudikoff S., Potter M.;

"Size differences among immunoglobulin heavy chains phosphorylcholine-binding proteins.";

Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
SEQUENCE ($107).

MEDLING-76110488; PubMed-813561;

Rudikoff S., Barstad P., Potter M.,

Unpublished results, cited by:

Hood L., Campbell J.H., Elgin S.C.R
                                                                                                                                                                                                    SEQUENCE FROM N.A. (H107).

MEDLINE-80199926; PubMed-676593;

Early P., Huang H., Davis M., Calame K.,

"An immunoglobulin heavy chain variable
three segments of DNA: VH, D and JH.";

Cell 19:981-992(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV18_MOUSE STANDARD; PRT; 123 AA. P01787; P01787; P01787; P1787; P17986 (Rel. 01, Created) P17-JUL-1986 (Rel. 01, Last sequence update) P17-JUL-1999 (Rel. 38, Last annotation update) P17-JUL-1999 (Rel. 38, Last annotation update) P18-JUL-1999 (Rel. 38, Last annotation update) P19-JUL-1999 (Rel. 38, Last an
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Proc. Natl. Acad. Sci. U.S.A.
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15-JUL-1999 (Rel. 38, Last an
IG HEAVY CHAIN V REGION H8.
HV22_MOUSE STANDARD; PRT; : P01791; P01791; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence up 15-JUL-1999 (Rel. 38, Last annotation IG HEAVY CHAIN V REGION HPCM6.
                                                                                                                                                                                                                                                                                  Barstad P.;
Thesis (1975), California Institute of Technology / Pasadena, U.S.-I- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (HPCM1: HPCM2 AND HPCM3).
MEDITNE=81197602: PubMed=7231520;
Gearhart'P.J., Johnson N.D., Douglas
"IgG antibodies to phosphorylcholine
their IgM counterparts.";
Nature 291:29-34(1981).
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Pfam; PF00047; ig; 1.
Immunoglobulin V region; Hybridoma.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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-!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM
HYBRIOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE
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RX MEDITARE-81197602; PubMed-7231520;

RX MEDITARE-81197602; PubMed-7231520;

RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;

RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;

RI TigG antibodies to phosphorylcholine exhibit more diversity than

RT their IgM counterparts.";

RI MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT

CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT

BINDS PHOSPHORYLCHOLINE.

DR PIR, A02070, AVMST5.

DR InterPro; IPR033006; -.

DR InterPro; IPR033006; -.

DR INTERPOOMAT, 1g; 1.

THEMINOGIODULIN V region; Hybridoma.

FT NON_TER 123 123

SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;
                                                                                                                                                             Query Match 95.9%; Score 94; DB 1; Length 123; Best Local Similarity 95.0%; Pred. No. 2.2e-07; Matches 19; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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15.583 Million cell updates/sec
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O9uc53 homo sapien
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| 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 45.9 | 46.4 | 46.9 | 46.9 | 51.0 | 51.0 | 52.0 | 52.0 | 52.0 | 52.0 | 52.6 | 55.1 | 56.1 |
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| Œ | 10 | <u>, , , , , , , , , , , , , , , , , , , </u> | 5 | ഗ | Ç, | v | u | 5 | _ | 2 | ผ | N | N | 2 | 4 | 4 | 4 | 11 | 11 | 4 | 4 | 4 | 4 | 4 | 11 |
| 8AXA6Ö | 023154 | 058581 | 077287 | Q9U5V2 | Q9U5x9 | Q9U5V9 | Q9V420 | Q9VBU5 | Q9YDM7 | Q9R471 | Q9R711 | P94207 | 054389 | Q9RHX6 | 043292 | Q9NSSO | Q9Y298 | Q9Z1C6 | 035444 | 095978 | 095973 | Q9UL75 | Q9Y3R3 | Q9UL73 | Q9QXE9 |
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ALIGNMENTS

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Matches 20; Conserv
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Mammalia; Eutheria; F
NCBI_TaxID=9606;
[1]
Q9UL72 PRELIMINARY; PRT;
Q9UL72;
01-MAY-2000 (TrEMBLrel. 13, Created)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                           PFAM; PF00047; 1g; 1.
NON_TER 1 18
NON_TER 118 118
SEQUENCE 118 AA; 1:
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EMBL; AF035023; AAD56259.1; -.
                                                                                                                                                                                                                                          INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                               fetus."
                                                                                                                                                                                                                                                                                                    Young D.C.;
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118 AA; 12843 MW;
                                                                                                                                   Conservative
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Primates;
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RESULT
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Best Local Similarity 95.0
Matches 19; Conservative
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Saptens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            MEDLINE=98277139; PubMed=9614934; Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                       Q9UL90;
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                                                                    1 EVQLVESGGGLVQPGGSLRL 20
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
NYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMI
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-9277139; PubMed-9614934;

Wu X., Llu B., Van der Merwe P.L.,

Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus."
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113 AA; 12437 MW;
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118 AA;
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llarity 100.0%;
Conservative 0;
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12872 MW;
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95.08;
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Pred. No. 1
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Matches 19; Conser
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MEDLINE-98277139; PubMed-9614934;
                                                                                                                        PFAM; PF00047; ig; 1.
                                                                                              SEQUENCE
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OSUL88:

OSUL88:

O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMEDIVATIVE)
EUNATYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                         Young D.C.;
                                                                                                                                                                       Myosin-reactive autoantibodies in rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Tilu B., Van der Merwe P.L.,
           1 EVQLVESGGGLVQPGGSLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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121 AA; 13154 MW;
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1.8e-06;
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Matches 18; Conserv
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"Human VH gene sequence.";
Submitted (NOV-1999) to the E'
EMBL; A8035288; BAA87067.1; -
HSSP; P01772; 2FB4.
INTERPRO; IPRO03006; -.
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
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Q9UL84;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
IMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                   fetus.";
Clin. Immunol. Immunopathol.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                  INTERPRO; IPR003006; -. PFAM; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                              EMBL; AF035030; AAD56266.1; HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
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1 VQLEESGGGLVQPGGSLRL 19
EVQLVESGGGVVQPGRSLRL 20
                       EVQLVESGGGLVQPGGSLRL 20
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122 AA;
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94.7%;
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                                                                                   Score 87; DB Pred. No. 1.8c
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                          87:184-192(1998).
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P SEQUENCE FROM N.A.

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

R "Cloning of cDNAs encoding for anti-white pine blister rust

"antibody (Mab 7, its light and heavy chains) and constructi

"I single chain antibody (scFV).";

"Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

"Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

"EMBL; AF152372; AAD40243.1; -.

"R HSSP; P01842; 7FAB.

"R INTERPRO; IPR003006; -.

"PFAM; PF00047; ig; 4.

"PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                         Query Match
Best Local S
Matches 16
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Best Local S
Matches 17
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Q9UL93;
01-MAY-2000
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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                                                                                                                   Local Similarity
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VQLQESGGGLVKPGGSLKL
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116 AA;
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437 AA;
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84.2%;
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Pred. No. 9e-0
1; Mismatches
                                                                                         Score 80; DB
Pred. No. 0.00
2; Mismatches
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white pine blister rust
chains) and construction
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0.00076;
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Matches 16; Conservative
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MEDLINE-96071149; PubMed-7475288;
Cao J., Vescio R.A., Rettig M.B., Hong C.H
Lichtenstein A.K., Berenson J.R.;
"A CD10-positive subset of malignant cells
myeloma using PCR with patient-specific im
Leukemia 9:1948-1953(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QV16 PRELIMINARY; PRT;
Q9QV16; Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last seque
Q1-OCT-2000 (TrEMBLrel. 15, Last annot
PROLACTIN-BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cohen H., Cohen O., Gagnon J.;
"Serum prolactin-binding protein (PRL-BP) of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95094032; PubMed-8000909,
                                                                                                                                                                                                                                                                                                                                       identified as IgG.";
C. R. Acad. Sci., III, Sci. Vie 317:293-298(1994).
HSSP; P01789; IMCP
SEQUENCE 15 AA; 1469 MW; 35ED2512FF3FA369 CRC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10118;
[1]
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01-NOV-1999
01-NOV-1999
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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ER 1 1
                                                                                                                                                                                                     . Similarity
15; Conserv
                                                                                                                                                                                                  Conservative
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Rodentia;
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                                                                                                                                                                                                                        Score 75; Pred. No.
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Sciurognathi; Muridae;
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                                                                                                                                                             Cohen L.S., Welt S., Old L.J., Barbas C., "The rabbit antibody repertoire as a nove of therapeutic human antibodies.",
J. Biol. Chem. 275:13688-13676 (2000).
EMBL; AF245503; AAF68450.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Q9NOW4;
Q9NOW4;
Q9NOW4;
Q1-OCT-2000 (TrembLrel. 15, Created)
Q1-OCT-2000 (TrembLrel. 15, Last sequence update)
Q1-OCT-2000 (TrembLrel. 15, Last annotation update)
ANTI-HUMAN A33 HEAVY CHAIN DOMAIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit),
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Lagomorpha; Leporida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell
"Isolation of a novel type of vascular cell
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
STINOHATA N., Demura T., Fukuda H.;
Shinohara N., Demura T., Fukuda H.;
Shinohara N., Demura T., Fukuda H.;
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01-MAY-2000
01-MAY-2000
01-OCT-2000
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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QLVESGGGLVQPGGSLRL
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P01607; 1REI.
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124
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83.3%;
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                             Score 70; DB Pred. No. 0.001; Mismatches
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Pred. No. 0.00
5; Mismatches
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Last annotation update
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                                                                                                                              96D2B29FE27C24C8
                                                                                                                                                                                                                                                                   Elia M., Gout I.,
Barbas C.F. III.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                novel source
                                                   DB 6;
0.0054;
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sing a phage display
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0.0027;
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                                                                    Length 124;
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                                                                                                                                                                                                                              Query Match 67.:
Best Local Similarity 93.:
Matches 14; Conservative
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Q9NOW6;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last annotation update)
ANTI-HUMAN A33 HEAVY CHAIN DOMAIN (FRAGMENT).
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NON_TER
SEQUENCE
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Rader C., Ritter G., Nathan S., Elia M., Gout I., Jungbluth A.A.,

Cohen L.S., Welt S., Old L.J., Barbas C.F. III.;

"The rabbit antibody repertoire as a novel source for the generation

of therapeutic human antibodies.";

J. Biol. Chem. 275:13668-13676(2000).

EMBL; AF245501; AAF68448.1; -.
                                                                                                                                                                                                                         syndrome cells.";
Hum. Reprod. 10:1694-1701(1995),
SEQUENCE 16 AA; 1626 MW; C9C5ED2512FF3FB9 CRC64;
                                                                                                                                                                                                                                                                     MEDLINE-96033130; PubMed-8582963; Shiraishi Y., Shiraishi Y., Yamamoto D., Hasegawa T., Kitamura W., Shiraishi Y., Shiraishi Y., Soma H.; Miki S., Tanaka T., Suzuki T., Soma H.; "Diagnostic relevance of abortion-associated human embryonic antigen expressed on the cell surface of tumour promoter-treated Bloom
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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3 QLMESGGGLVTLGGSLKL 20
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Post-processing: Minimum Match 0%
Maximum Match 100%
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/AB_COMB.pep:*
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US-08-471-282A-80
US-08-466-710C-80
US-08-466-739C-0
US-08-468-739C-116
US-08-428-139-1
US-08-655-202-31
US-08-428-197-3
US-08-428-197-3
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US-08-98-352B-12
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118, Appl
119, Appl
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: KIT, GORDON

REGISTRATION NUMBER: 30,764

REFERENCE/DOCKET NUMBER: A-6901

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 293-7060

TELEPAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 anino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: beptide

HYPOTHETICAL: NO

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US-08-859-931A-2
                                                                                    Query Match
Best Local S
Matches 20
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,931A
FILING DATE: 21 MAY 1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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ADDRESSEE: SUGHRUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FASANO, Alessio TITLE OF INVENTION: SUBSTANTITLE OF INVENTION: PHYSIOI TITLE OF INVENTION: MAMMAL!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2100 Pennsylva CITY: Washington, D.C. STATE: D.C.
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                                                                                                            Similarity
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US-08-545-809A-23
US-08-804-444A-9
US-08-80-107-669D-23
US-08-172-788A-23
US-08-477-531B-23
US-08-68-201-2
US-08-988-201-4
US-08-988-201-4
US-08-988-201-4
US-08-988-113B-159
US-08-6488-113B-159
US-08-646-360-159
US-08-646-360-159
US-08-934-373C-2
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Pred. No. 2.9e-08;
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length:

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US-08-467-282B-80
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ORGANISM:
US-08-471-780C-80
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INFORMATION FOR SEQ ID NO: 80
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                     Sequence 80, Application US/08467282B Patent No. 5800988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-471-780C-80
     GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
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Best Local
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FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 934
FILING DATE: 21-MAY-1993
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ORIGINAL SOURCE:
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
APPLICATION NUMBER: 17-AUG-1993
The Pr 92402326.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
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APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         Local Similarity es 20; Conserv
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06-JUN-1995
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                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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US-08-471-282A-80
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Best Local
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                                                                                            APPLICANT: Casterman, Cecil
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immuno;
NUMBER OF SEQUENCES: 130
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                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/106,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                   STATE: D.C
                                                 STREET:
COUNTRY:
                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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STREET: 1300 I St
CITY: Washington
STATE: D.C.
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 01
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 9:
FILING DATE: 21-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20005-3315
                                 Washington
                                        E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W.
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   USA
                                                                                                                                                 Casterman, Cecile
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1300 I Street, N.W.
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linear
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                                                                                                          Immunoglobulins Devoid of Light Chains
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4000
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                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 9
FILING DATE: 21-AUG-1992
                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Casterman, Cecile APPLICANT: Hamers, Raymond TITLE OF INVENTION: Immunoglo
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                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                      CLASSIFICATION:
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STRANDEDNESS: sin
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                                                                                                                                                       FILING DATE:
                                                                                                                                                                    APPLICATION NUMBER: US/08/466,710C
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20005-3315
                                                                                                                                                                                                                                                                                                                                            Washington
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1300 I Street, N.W.
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06-JUN-1995
MBER: FR 93401310.3
21-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulins Devoid of Light Chains
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                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                  US/08/106,944
                                                                  FR 92402326.0
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                       TELEFAX: 202-408-4400
                                                        SEQUENCE CHARACTERISTICS
                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                APPLICATION NUMBER: FR 93401310. FILING DATE: 21-MAY-1993 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglo
NUMBER OF SEQUENCES: 130
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                                                                                                                                                                                                                                    APPLICATION NUMBER: FR 92
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93
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                                                                                                                                              NAME: POTTER, Jane E.R. REGISTRATION NUMBER: 33,332 REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/106,944 FILING DATE: 17-AUG-1993 APPLICATION NUMBER: FR 92402326.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/468,739C FILING DATE: 06-JUN-1995 CLASSIFICATION: 530
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REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
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TYPE: amino acid
STRANDEDNESS: single
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6015695
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1300 I Street, N.W.
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linear
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MOLECULE TYPE: ORIGINAL SOURCE:

protein

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                                                                                                                                                                                                                                            US-08-211-202-116
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Best Local Similarity
                                                                                                                                                                                                           Sequence 116, Appl Patent No. 5565332
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                 APPLICANT:
                                                                            CORRESPONDENCE ADDRESS:
                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                      PPLICANT:
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TOPOLOGY: lir
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                               STREET:
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                                                                                                                                                                                              INFORMATION:
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Chicago
: Illinois
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                               6300 Sears Tower, 233 South Wacker Drive
                                                                                                     JESPERS, Laurent Stephane Anne Therese WINTER, Gregory Paul NVENTION: Production of chimeric antibon NVENTION: combinatorial approach
                                                                                                                                                                                                                           Application US/08211202
                                                                                                                                                                  BAIER, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sSS: single
linear
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                                                           David W. Clough, Marshall O'Toole Gerstein Murray
                                              Borun
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Pred. No.
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                                                                                                        chimeric antibodies - approach
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hes 0;
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                            Sequence 37,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,20
FILING DATE: 23-SEP-1992
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MEDIUM TYPE: Floppy disk
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LENGTH: 98 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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APPLICATION NUMBER:
FILING DATE: 24-MAR-
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FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
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                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                        TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                     APPLICANT:
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ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: David W. Clouder REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
APPLICATION NUMBER: PCT/
PTT.TNG DATE: 15-MAY-199
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                                       STREET: 2100 Pension CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid TOPOLOGY: linear
                              STATE:
                                                        ADDRESSEE: Sughrue, Mion, STREET: 2100 Pensylvania
           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGGLVQPGGSLRL 20
                                                                                                                                                                                                                                                  7, Application US/07942245 5639641
RY: United States 20037-3202
                             D.C
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SEARLE,
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                    REES,
                                                                                                                                                                      ROGUSKA,
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SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES
522
                                                                                                                                                                                   Stephen M.J
Anthony R.
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                                                                                                                                                                       Michael
                                                                                                                                                                                                                  Jan T.
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                                                            Zinn, Macpeak & Seas
Avenue, N.W.
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Pred. No.
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COMPUTER:

HP 9000/700 Workstation

OPERATING SYSTEM: MEDIUM TYPE:

UNIX

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                                                                                                                                                                             APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Marks,
APPLICANT: Schier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 98 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEPAX: (202) 293-7860
TELEX: 6491103
                                                                                     NAME: HUNTER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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CURRENT APPLICATION DATA:
US/07/942,245
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                       TELEPHONE:
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California
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                                                                       (415) 576-0200
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100.0%; Pr
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Pred. No.
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thes 0;
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-31
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US-08-428-197-4
                                               Query Match
Best Local S
Matches 20
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GENERAL INFORMATION:
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Best Local Similarity
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TELEFAX: (619) 455-51
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US93/10555
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-0CT-1993
ATTORNEY_AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: SFL
                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
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ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                          NAME/KEY:
LOCATION:
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CITY: Los Angeles
STATE: California
                                               Match 100.0%;
Local Similarity 100.0%;
les 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IE
                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
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1 EVQLVESGGGLVQPGGSLRL 20
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                                                                                                                                                                                                                                                                                  108 amino acids
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linear
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Pred. No. 1.5e-07;
                                                            Score 98; DB 2;
Pred. No. 1.7e-07;
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                                                                                                                              Sequence 3, Application US/08428197 Patent No. 5891438 GENERAL INFORMATION:
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Best Local :
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GENERAL INFORMATION:
                                           APPLICANT: SILVERMAN TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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TOPOLOGY: lin
MOLECULE TYPE:
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NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                 CORRESPONDENCE
                               NUMBER OF SEQUENCES:
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FILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide LOCATION: 1..108
                                                                                                                                                                                                                                                  1 EVQLVESGGLVQPGGSLRL 20
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1880 Century Park East - Suite 500
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Spensley Horn Jubas & Lubitz
               ADDRESS
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                                                         METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
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                                                  THEREOF
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PCT-US93-10555-3
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                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application PC/TUS9310555 GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
OPERATING SYSTEM: PC-DOS_MS-DOS
                                                                                                                                              STREET: 1000
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5110
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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IMMEDIATE SOURCE:
CLONE: Huabl4-
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APPLICATION NUMBER: PCT
FILING DATE: 29-OCT-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRL 20
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California
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1880 Century Park East - Suite 500
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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29-OCT-1993
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                                                                                                                                                                                                                                                                            METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                                                                                                                                                                                                  THEREOF
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Pred. No. 1.7e-07;
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CLASSIFICATION: ATTORNEY/AGENT INFORMATION:

FD-2630

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US-08-974-899-6
US-08-974-899-6
; Sequence 6, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
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Best Local Similarity
Thes 20; Conserve
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; LOCATION:
PCT-US93-10555-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HOWELLS, STACY L.

REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 anino acids
                    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                         NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0:
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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Query Match
Best Local Similarity
Matches 20; Conserv
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100.0%; Score 98; DB 3; 100.0%; Pred. No. 1.8e-07; Live 0; Mismatches 0;
                          Length 113;
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 0;
 Gaps
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δõ 밁 1 EVQLVESGGGLVQPGGSLRL 20 EVQLVESGGGLVQPGGSLRL 20

Search completed: June 13, 2001, 14:27:07 Job time: 628 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /SIDS6/gcgdata,
2: /SIDS6/gcgdata,
3: /SIDS6/gcgdata,
4: /SIDS6/gcgdata,
5: /SIDS6/gcgdata,
6: /SIDS6/gcgdata,
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Y79131
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Y41168
Y49069
Y31769
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                  Human adult brain
Human adult brain
Llama Vhh polypept
Recombinant alpha
Llama Vhh polypept
T84.12 Heavy chain
chiT84.12 H3 heavy
Anti-melanoma anti
Llama Vhh polypept
Amino acid sequenc
                                                                                                                                                                                                                                                                                                     Description
Staphylococcus
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W94488
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| Bac Hal Hal DJH Part | Syn Syn Ami Cry Tru B. | | | W H H O W K F ; |
| lus thuringi length hybri length hybri gene product l sequence o | etic Bacillu etic Bt endc acid sequen (c) crystal ated insecti | s thuringi of the Ba elta-endot s thuringi ic Bacillu ic Bt endo s thuringi | MONOCIONAL MILLION H. pylori GHPO 140 Open reading frame Streptococcus pyog Chlamydia pneumoni Bacillus thuringie Bruncated modified Truncated modified Cryla(b)[5.3] toxi | Staphylococcus aur Human secreted pro Human secreted pro Clone selected aft SYNTHE-9 Bt2 modif Monoclonal antibod Protein which is s |

ALIGNMENTS

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Zonulin; mammalian tight junction; zonula occludens toxin; ZOT; Vibrio cholerae; vaccine; cholera toxin; polyclonal antibody; intestinal mucosa; nasal mucosa; blood brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adult brain zonulin N·terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1999 (first entry)
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                                                (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                21-MAY-1997;
                                                                                                                                             28-APR-1998;
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Claim

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Page 45;

64pp;

English

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Best Local S
Matches 9
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                                          New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                      Zonulin; antagonist; zonula occludens toxin receptor; human; blood-brain barrier; antiinflammatory; gastrointestinal inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes pure zonulin which has an apparent molecular weight of 47 kD, as determined by SDS-PAGE, which is recognised by both anti-tau polyclonal antibody and by anti-zonula occludens toxin (ZOT) polyclonal antibody, and is capable of reversibly opening mammalian tight junctions. Zonulin proteins function as physiological modulators of mammalian tight junctions. They can be used for enhancing the absorption of therapeutic agents across tight junctions of intestinal and nasal mucosa and across tight junctions of the blood brain barrier. Zonulin can be used with agents such as drugs,
         Example 3; Fig 6; 69pp; English
                                                                                                                     WPI; 2000-205565/18
                                                                                                                                                                                                                                03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2000 (first entry)
                                                                                                                                                                                          (UYMA-) UNIV
                                                                                                                                                                                                                                                                                                                                        WO200007609-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human adult brain zonulin N-terminal sequence
                                                                                                                                                                                                                                                                   28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y79131 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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1 vtfytdavs
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llarity 100.0%;
Conservative (
                                                                                                                                                                                            MARYLAND BALTIMORE
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                                                                                                                                                                                                                                98US-0127815
                                                                                                                                                                                                                                                                 99WO-US16683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 20;
Pred. No. 3.2e+05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
lymphocyte activation. Purceive to inhibit lymphocyte activation by blocking delivery to inhibit lymphocyte activation. Purceive the products are useful for inhibit lymphocyte activation by blocking delivery to limphocyte activation by blocking delivery to l
                                                                                                                                                                                                      The invention relates to a method of regulating lymphocyte activation by selectively binding multiple cell surface (mcs) antigens expressed the same lymphocyte. The method and the products are used to regulate lymphocyte activation. Lymphocytes can be incubated with immobilized ligands or Ab's or their fragments specific for the target Ag's in ord to achieve Ag aggregation in vitro. The multispecific molecules that contain multiple binding specificities in a single soluble molecule are
                                                                                                                                especially useful in aggregating multiple Ag's in vivo resulting in lymphocyte activation. Multispecific molecules may also be constructed to inhibit lymphocyte activation by blocking delivery of activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulation of lymphocyte activation using, molecules, used for treatment of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lymphocyte; multiple cell surface; antigen; ligand; T cell response; B cell response; immune enhancement; immunosuppression; immunotherap cancer; infectious disease; multiple surface receptor; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of the N-terminal region of adult human brain zonulin. The N-terminal sequences of human adult and foetal zonulins (see Y79130-36) were compared with Vibrio cholerae zonula occludens toxin (ZOT) to identify a common motif thought to be involved in receptor binding. Peptide antagonists (see Y79105-29) based on this motif are useful as antiinflammatory agents for treatment of gastrointestinal inflammation, and for treatment of conditions associated with breakdown of the blood-brain
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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16-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XCYT-) XCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Llama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 16A; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide hybrid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THERAPIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayden Ledbetter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0075274.
98US-0108683.
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                                                                              responses in vivo and in vitro. The activation
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.2e+05;
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Best Local :
The recombinant enzyme was produced by cloning the gene encoding it from a C. thermohydrosulphuricum genomic library and using it to express the enzyme in a host cell e.g. E.coli which is easier to cultivate and has less complex nutritional requirements than C. thermohydrosulphuricum ( which is an obligate anaerobic thermophilic organism). The enzyme is used to hydrolyse starch, amylase or pullulan, opt. in conjunction with a glucogenic or maltogenic enzyme. It has an optimum temp. range of 80-85 deg.C, i.e. 5 deg. lower than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expanded T and/or B cells are used in adoptive immunotherapy of cancer and infectious diseases such as AIDS. Aggregation of multiple surface receptors or inhibition of lymphocyte activation is not only limited to treatment of, e.g. immunodeficiency, infectious diseases and cancer and can also be applied for a wider variety of treatments such as for suppression of autoimmunity, hypersensitivity, vascular disease and transplant rejection. Also, stimulation of human T cells with immobilized Ab's specific for three T cell surface Ag's results in enhanced proliferation when compared with stimulation by two immobilized Ab's. Sequences Y41165-73 represent Llama Whh polypeptide unique hybrid sequences, Y41174-79 represent Llama Whh complete sequences and Y41180-85
                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                      Heat stable enzyme with both alpha-amylase and pullulanase activities - prepd. by expressing Clostridum thermohydrosulphuricum DNA in host cells, useful in hydrolysis of starch, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1990;
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                                                                                                                                                                                                                                                                              6; Fig 5; ]27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R08221.
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85.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liquefaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Best Loc
Matches
                                                                                                                                                                                                                The invention relates to a method of regulating lymphocyte activation by selectively binding multiple cell surface (mcs) antigens expressed the same lymphocyte. The method and the products are used to regulate lymphocyte activation. Lymphocytes can be incubated with immobilized ligands or Ab's or their fragments specific for the target Ag's in orde to achieve Ag aggregation in vitro. The multispecific molecules that contain multiple binding specificities in a single soluble molecule are especially useful in aggregating multiple Ag's in vivo resulting in lymphocyte activation. Multispecific molecules may also be constructed to inhibit lymphocyte activation by blocking delivery of activation signals to the cells. The methods and the products are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that of the native enzyme, least 10 differently sized activities were produced, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B cell response; immune enhancement; immunosuppression; immunotherapy; cancer; infectious disease; multiple surface receptor; AIDS; hypersensitivity; vascular disease; transplant rejection; Vhh protein.
                            and infectious diseases such as AIDS. Aggregation of multiple surface receptors or inhibition of lymphocyte activation is not only limited treatment of, e.g. immunodeficiency, infectious diseases and cancer ar can also be applied for a wider variety of treatments such as for
                                                                                                                                      Expanded T and/or B cells are used in adoptive immunotherapy of cancer
                                                                                                                                                             regulation of T and B cell responses in vivo and in vitro. The activation of signals may result in either immune enhancement or immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 43; Fig 16A; 114pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulation of lymphocyte activation using, e.g. multispecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-FEB-1998;
16-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9942077-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Llama llama.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y41166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y41166 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Llama Vhh polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (XCYT-) XCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 itfyydsvs 230
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6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used
applied for a wider variety of treatments such as for of autoimmunity, hypersensiting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THERAPIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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98US-0108683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surface; antigen; ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB Pred. No. 3.2e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzymic
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                                                         limited to cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Law
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R47450
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         Query Match
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Matches 5
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                           tumour marker carcinoma embryonic antigen, and is useful for tumour imaging and immunotherapy.

The amino acid sequence given in the specification has been incorrectly identified as a nucleic acid sequence, therefore unacceptable characters have been represented as an 'N'.

The amino acid sequence given below has been derived from the cDNA, by the indexer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences (Q54651-52) show the light of murine T84.12. The T84.12 antibody is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 17; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimaeric {\tt T84.12} antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-007204/01.
N-PSDB; Q54652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric; carcinoembryonic antigen; CCA; murine; mouse; region; transform; myeloma cell; light chain; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T84.12 Heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplant rejection. Also, stimulation of human T cells with immobilized Ab's specific for three T cell surface Ag's results in enhanced proliferation when compared with stimulation by two immobilized Ab's. Sequences Y41165-73 represent Llama Whh polypeptide unique hybrid sequences, Y41174-79 represent Llama Whh complete sequences and Y41180-85 represent Llama constant region sequences.
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R47450 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1992;
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itfyadsv 62
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         Similarity 62.1
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ϋ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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2; Mismatches 1;
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Best Local S
Matches 5
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The amino acid sequence given in the specification has been incorrectly identified as a nucleic acid sequence, therefore unacceptable characters have been represented as an 'N'. The amino acid sequence given below has been derived from the cDNA, by the indexer.
                                                  W13514;
                                                                                               W13514
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimaeric T84.12 antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also DNA encoding it and transformed myeloma cells
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Yang YH;
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DB; Q54655.
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5; Conserv
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cell; light chain; tumour.
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2.3e+02;
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28-OCT-1997

(first entry)

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RESULT
Y41168
ID Y4
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 19; Page 52; 82pp;
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Y41168 standard; protein;
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The invention relates to a method of regulating lymphocyte activation CC by selectively binding multiple cell surface (mcs) antigens expressed by Ct the same lymphocyte. The method and the products are used to regulate CC lymphocyte activation. Lymphocytes can be incubated with immobilized CC ligands or Ab's or their fragments specific for the target Ag's in order CC expecially useful in aggregation in vitro. The multispecific molecules that CC contain multiple binding specificities in a single soluble molecule are CC expecially useful in aggregating multiple Ag's in vivo resulting in CC lymphocyte activation. Multispecific molecules may also be constructed to inhibit lymphocyte activation by blocking delivery of activation CC signals to the cells. The methods and the products are useful for regulation of T and B cell responses in vivo and in vitro. The activation of signals may result in either immune enhancement or immunosuppression. Expanded T and/or B cells are used in adoptive immunotherapy of cancer CC and infectious diseases such as AIDS. Aggregation of multiple surface conceptors or inhibition of lymphocyte activation is not only limited to treatment of, e.g. immunodeficiency, infectious diseases and cancer and CC suppression of autoimmunity, hypersensitivity, vascular disease and CC and also be applied for a wider variety of treatments such as for CC sequences Y41165-73 represent Llama vhh polypeptide unique hybrid CC represent llama constant region sequences.

CC represent Llama vhh complete sequences and Y41180-85 cc represent Llama vhh complete sequences and Y41180-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulation of lymphocyte activation using, e.g. multispecific molecules, used for treatment of cancer - \,
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                  sequences, Y41174-79 represent I
represent Llama constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 43; Fig 16A; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-633594/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1998;
16-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09942077-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Llama llama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymphocyte; multiple cell surface; antigen; ligand; T cell response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Llama Vhh polypeptide hybrid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y41168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XCYT-) XCYTE
                                     Local
   Similarity
5; Conserv
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THERAPIES INC
                                                                                                                                                                        Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayden Ledbetter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0075274.
98US-0108683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US03309
                                     68.9%;
Score 31; DB 20;
Pred. No. 1.5e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĭ
                                                                                                                                                                                                                                      sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brady WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grosmaire LS,
                                                                 Length 208
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ımmunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vhh protein
      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Law
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ç
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망
                                   S
                                                                                                                                                                            DNA molecules from Gram positive bacterium, corresponding to dnaE

C (231001), dnaX (231002), and dnaB (231003). The POIC, dnaN and dnaG genes

C (231004-231006) are also identified. The dnaE gene corresponds to the

C alpha subunit of the Escherichia coli, DNA polymerase III holoenzyme,

C dnaX corresponds to the gamma and tau subunits, and dnaB corresponds to

C the helicase. The alpha subunit is the actual DNA polymerase, the gamma

CC complex forms the clamp loader and tau is a "glue protein". DnaX encodes

CD both gamma and Tau, Tau is the product of the full gene, while gamma is

CC the product of the first two thirds of the gene. The DNA sequences of the

CC replication by acting on various parts of the gram positive bacterial DNA

CC replication by acting on various parts of the gram positive bacterial DNA

CC colymerase holoenzyme. The products and methods of the invention can be

CC used for identifying pharmacological agents or lead compounds for agents

CC active at the level of a replication protein function, particularly DNA

CC replication. The agents identified can be used as antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
Y49069
                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence encoded by the partial dnaB gene (231003) of Staphylococcus aureus. The invention relates to a number of isolated
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; Page 21-25; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated dnaE, dnaX and dnaB genes from Gram positive bacteria, used to develop screening assays for identifying antibiotic compoun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-590685/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Donnell ME,
102 vqyytdivs 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1998;
22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09937661-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gram positive bacteria; dnaE; dnaX; dnaB; PolC; dnaN; dnaG; helicase; alpha subunit; DNA polymerase III holoenzyme; gamma subunit; tau subu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y49069 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence encoded by partial dnaB gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y49069;
                   1 VTFYTDAVS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         loader; glue protein; replication; antibiotic.
                                                                                                                                                     457 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0074522
98US-0093727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US01547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by ACAGGC
                                                                                    68.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whipple R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457
                                                                                Score 31; DB 20;
Pred. No. 3.5e+02;
                                                                    Mismatches
                                                                                                Length 457;
                                                                Indels
                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tau subunit;
                                                             Gaps
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RESULT 11

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RESULT 12
Y70133
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                                                                                                                     В
                                          IJ
                                                                                                                                                                                                                                                                                      This sequence represents the replicative helicase, dnaB, of Staphylococcus aureus strain WCUH 29 (NCIMB 40771). The sequence Was deduced from an isolated polynucleotide (see X87985) and shows Structural homology to other proteins of the replicative helicase C family. The invention provides dnaB polynucleotides and polypeptides, and methods for producing such polypeptides by recombinant techniques. Also provided are methods for utilising C dnaB polypeptides to screen for antibacterial compounds, especially C those that target antibiotic-resistant strains. The polypeptides C and polynucleotides may be employed as research reagents for the C discovery of treatments and diagnostics, particularly for human C discases. The polypeptides can be used to produce antibodies, of Hese are used to prevent, inhibit or treat diseases, particularly C of Helicobacter pylori infections, such as gastrointestinal can also be used to treat wounds and in-dwelling devices to prevent c bacterial adhesion and infection, and to block dnaB protein-mediated mammalian coll invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                         Query Match
            Y70133
                                      Y70133 standard; Protein; 466 AA.
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                    mammalian cell invasion.
                                                                                                                  102 vqyytdivs 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 46-47; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel replicative helicase dnaB polynucleotides and polypeptides Staphylococcus aureus used to screen for antibacterial compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-561656/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              мау ЕW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus replicative helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09946275-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Replicative helicase; dnaB; antibacterial; antibiotic; screening; infection; bacteraemia; sepsis; therapy; diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y31769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y31769 standard; Protein; 466
                                                                                                                                                1 VTFYTDAVS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Earnshaw DL,
                                                                                                                                                                                                                                                       466 AA;
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0038909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US05286.
                                                                                                                                                                                             68.9%;
                                                                                                                                                                          Score 31; DB ZU; _
Pred. No. 3.5e+02;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dnaB
                                                                                                                                                                                                        Length 466;
                                                                                                                                                                           Indels
                                                                                                                                                                           0;
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of.
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RESULT
B33998
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                                                                                                                                                                                             DXXXX
                                                                                              밁
                                                                                                                                        Matches
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      The present sequence is a replicative DNA helicase DnaB from Staphylococcus aureus genomic DNA library.

The present sequence is useful in preparation of vaccines for prevention or attenuation of Staphylococcal infections (especially prevention or attenuation of Staphylococcal infections).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; antibacterial; prevention; attenuation; detection; Staphylococcal infection; neonatal conjunctivitis; skin infection; toxic shock syndrome; osteomyelitis; DnaB; replicative DNA helicase
 02-FEB-2001
                      в33998;
                                                                                                                                                                                                                                                                                                                Claim 9; Page 12; 144pp;
                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus polypeptide useful for preventing or attenuating a Staphylococcal infection comprises one of 32 sequences of 100-1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-2000.
                                         B33998 standard;
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                         S.aureus infections) which may cause conditions such as neonatal conjunctivitis, osteomyelitis, skin infections and toxic shock syndrome. The present sequence is also useful for detecting Staphylococcal
                                                                                                                                                                                                                                                                                                                                     amino acids or their fragments -
                                                                                                                                                                                                                                                                                                                                                                                                               Bailey CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200012678-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                The present sequence is also useful for infections in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                              102 vqyytdivs 110
                                                               13
                                                                                                                   1 VTFYTDAVS 9
                                                                                                                                                                                                                                                                                                                                                                                 2000-237864/20.
DB; Z51218.
                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN GENOME SCI
                                                                                                                                        6,
                                                                                                                                                                                             466
                                                                                                                                                                                                                                                                                                                                                                                                               Choi GH;
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
(first entry)
                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0098964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US19726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aureus replicative DNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- .
178..181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label-
411..416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Antigenic_epitope
304..306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label•
                                         Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 403
                                                                                                                                                   68.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l= Antigenic_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigenic_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _Antigenic_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigenic_epitope
                                                                                                                                                                                                                                                                                                                English.
                                          37
                                                                                                                                      Score 31; DB 21;
Pred. No. 3.5e+02;
1; Mismatches 2
                                          ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DnaB
                                                                                                                                                          Length 466
                                                                                                                                      0
                                                                                                                                      Gaps
                                                                                                                                      0;
RESULT
Y41320
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                                                                                                                                                                                Query Match
Best Local S
Matches 6
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Human; secreted protein; fusion protein; gene therapy; protein therapy;

Human secreted protein encoded by gene 13 clone HMSKI86

02-DEC-1999

(first entry)

Y41320 standard;

Protein;

48

14

18

26

VTFYTDAVS 9 ltlytdfvs

Similarity 6; Conser

Conservative

66.78;

Score 30; DB Pred. No. 36; 1; Mismatches

2

0

Gaps

0

Length 37; Indels

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Sequences B33963-B34006 represent the amino acid sequences of 48 human secreted proteins encoded by the genes C59392-C59439. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast an ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antilinfamatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord neurological disease; infection; human; secreted protein.
                                  ischaemias; (d) wound healing; (e) neurological diseases anoxia and epilepsy; and (f) infectious diseases such as bacterial, fungal and parasitic infections.
                                                                                              Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial
                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 370; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1999;
08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000; 2000WO-US06823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200056765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein encoded by cDNA #39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-602215/57.
  37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0125364
99US-0169623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                            cerebral
                                                                                                                                                                                                                  1 in
and
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Matches
                                                                   Query Match
Best Local
                                                                                                                                                                  as compared to the human protein only.

The invention relates to 95 novel genes and their fragments (nucleic acid sequences: 224811-224907; amino acid sequences Y41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 95 polynucleotides, based on
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01-APR-1998;
01-APR-1998;
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19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                                                                                                                               This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. Z24802) for increasing the stability of the fused protein
                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                    disorders
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19-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; lumnune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
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DB; Z24823.
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יימח RD,
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The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand, and then screening selected functional polypeptides with a target ligand. The method comprises contacting a permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides which are functional, well folded represent clones selected after panning primary and somatic NNK libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
Sequence
                                                                                                                                                                                                                                                                       Screening for functional polypeptides which
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20-OCT-1997;
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enrichment;
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single chain antibody; ScFv.
                       hen egg
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Copyright (c) 1993 - 2000 Com
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| C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_ | RESULT 1 A84066 molybdenum | | ٠ | 45 | 44 | 43 | . 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | |
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| re. | ₫ | | | <i>ا</i> | N | Ν | N | N | N | N | Ν | N | N | N | N | N | N | N | Ν | |
| vision 01-Dec-20 | ybdate-binding p | ALIGNMENTS | | JD0002 | A26513 | T01105 | C72725 · | G81727 | T03095 | S11445 | T23922 . | A70954 | T11659 | T11489 | JC6561 | T25235 | D64547 | A71960 | н70937 | |
| halodurans #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000 | transport system (molybdate*binding protein) BH3329 [imported] - Bacillus | | | parasporal crystal | parasporal crystal | disease resistance | hypothetical prote | conserved hypothet | homeoprotein Sail | parasporal crystal | hypothetical prote | hypothetical prote | hypothetical prote | NADH dehydrogenase | UDP-N-acetylmuramo | hypothetical prote | iron-sulfur cofact | probable nitrogena | hypothetical prote | |

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A;Molecule type: DNA
A;Residues: 1-365 <STO>
A;Cross-references: GB:AP001513; GB:BA0000004; NID:g10174345; PIDN:BAB05602.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                      hypothetical protein BH1883 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (c;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000 C;Accession: C83885 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 200. A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20263314 A;Accession: C83885
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C83885
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C;Superfamily: molybdate-binding periplasmic protein
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A;Residues: 1-260 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07048.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                                 A; Gene: BH1883
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192 IVFYTDALS 200
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les 6; Conservative
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    75.6%;
66.7%;
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    Score 34;
Pred. No.
DB
24;
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                          Length 365;
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A; Pathway: g
C; Superfamil
C; Keywords:
    A:Description: catalyzes the hydrolysis of internal A:Pathway: glycogen/starch degradation C:Superfamily: alpha-amylase core homology C:Keywords: glycosidase; hydrolase; multifunctional
                                                                                                                                                                                                                                               A:Cross-references: EMBL:M97665; NID:g144719; PIDN:AAA23201.1; PID:g144720 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July A:Note: the source is designated as Thermoanaerobacter thermohydrosulfuricus F:Mathupala, S.P.; Lowe, S.E.; Podkovyrov, S.M.; Zeikus, J.G. J. Biol. Chem. 268, 16332-16344, 1993 A:Title: Sequencing of the amylopullulanase (apu) gene of Thermoanaerobacter A;Reference number: A47341; MUID:93346376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amylopullulanase precursor [validated] - Thermoanaerobacter ethanolicus (strain 39E) N;Contains: alpha-amylase (EC 3.2.1.1); alpha-dextrin endo-1,6-alpha-glucosidase (EC C;Decies: Thermoanaerobacter ethanolicus C;Dete: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 03-Nov-2000 (Accession: S28669; A47341 R;Mathupala, S; Saha, B.C.; Zeikus, J.G. Biochem. Biophys. Res. Commun. 166, 126-132, 1990 A;Title: Substrate competition and specificity at the active site of amylopullulanase A;Reference number: S28669; MUID:90147689
                                                                                                          A; Gene: apu
A; Start codon:
                                                                                                                                                      A; Molecule type: DNA A; Residues: 1-1481 <A A; Cross-references: CC; Genetics:
                                                                                       C; Function:
                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1481 <MAT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic A;Pathway: glycogen/starch degradation C;Superfamily: fibronectin type III repeat homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-amylase (EC 3.2.1.1) / alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) (Species: Thermoanaerobacter thermohydrosulfuricus C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 15-Oct-1999 C;Accession: A44765 R;Melasniemi, H.; Paloheimo, M.; Hemioe, L. J. Gen. Microbiol. 136, 447-454, 1990 A;Title: Nucleotide sequence of the alpha-amylase-pullulanase gene from Clostridium A;Reference number: A44765; MUID:90362027 A;Accession: A44765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1475 <MEL>
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: GB:M97665;
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                                                                                                                                                        NID:9144719; PIDN:AAA23201.1; PID:9144720
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Pred. No. 97;
2; Mismatches
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97;
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                                                        1,4-alpha-D-glucosidic
  enzyme;
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                                                                                                                                                                                                                                                                                                                                                                        R; Wamsley, P.; Kramer, J. submitted to the EMBL Data Library, December 1996 A; Description: The sequence of C. elegans cosmid A; Reference number: 220116
                                                                                                                                                                                         A; Introns:
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A; Residues: 1-651 <WAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caenorhal
C;Date: 15-Oct-1999
C;Accession: T25953
                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                            A; Gene: CESP: ZC204.8
                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T25953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ZC204.8 - Ca
C; Species: Caenorhabditis elegans
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Best Local Similarity
"---has 6; Conserv?
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A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-474 <KAW>
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B75126
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                                                                                                              Query Match
Best Local
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                                   | TFYTDAV
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66.7%;

    Caenorhabditis elegans

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Pred. No.
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Pred. No.
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archaeal chromosome

20-Jun-2000

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CESP: ZC204

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C;Accession: C64765
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pern A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Accession: C64765
                                   3-oxoacid CoA-transferase (EC 2.8.3.5) precursor, mitochondrial [validated] - C;Species: Sus scrofa domestics (domestic pig) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 26-May-2000 C;Accession: A41771; S27952 R;Lin; T.W.; Bridger, W.A. J. Biol. Chem. 267, 975-978, 1992
                                                                                                                                                                 RESULT
A41771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T27B3.60 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change C;Accession: T46113 R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
T46113
    J. Biol. Chem. 267, 975-978, 1992
A; Title: Sequence of a cDNA clone encoding
A; Reference number: A41771; MUID:92112838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-486 <BLAT>
A;Cross-references: GB:AE000144; GB:U00096; NID:g1786568;
A;Experimental source: strain K-12, substrain MG1655
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A; Residues: 1-695 <NYA>
A; Cross-references: EMBL: ALL137079
A; Experimental source: cultivar Co
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C; Species: Escherichia coli
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A; Introns: 20/3;
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A; Accession: T46113
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F;29-486/Product:
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                                                                                                                                                                                                                                                                                         3 FYTDAV
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                                                                                                                                                                                                                                                 FYTDAV 144
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7B3.60
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6; Conser
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ct: yaiT protein #status
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                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107/2; 144/1; 228/3;
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                                                                                                                                                                                                                                                                                                                                                71.1%;
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Pred. No.
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No.
                     pig
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82;
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                       heart mitochondrial CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                                <SIG>
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                                                                                                                                                                                                                                                                                                                                                                     Length 486
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                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAC73474.1; PID:g1786569
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                                                                                                                                                                                                                                                                                                                             0
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A;Reference number: A69000; MUID:98037514
A;Accession: H69201
A;Status: preliminary; nucleic acid seque
                                                      ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierz ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium
                                                                                                                                                             hypothetical protein MTH762 - Methanobacterium thermoautotrophicum (strain | C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000 C;Accession: H69201
                                                                                                                     R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan
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preliminary; nucleic acid sequence

not shown; translation not shown

thermoautotrophicum Delta

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Reeve,

Jiwani,

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(strain Delta

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R.; Wang, Y T : Mao, J.;

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A; Accession: A41771
A; Molecule type: mRNA
A; Residues: 1-520 <LIN>
A; Cross-references: EMBL:M80534; NID:g164422; PIDN:AAA31019.1; PID:g164423
A; Cross-references: EMBL:M80534; NID:g164422; PIDN:AAA31019.1; PID:g164423
A; Experimental source: heart
A; Note: sequence extracted from NCBI backbone (NCBID:75613)
A; Note: parts of this sequence, including the amino end of the mature protein.
C; Function:
C; Function: EC 2.8.3.5 [validated; MUID:92112838]
A; Description: EC 2.8.3.5 [validated; MUID:92112838]
C; Superfamily: 3-oxoacid COA-transferase; 3-oxoadipate COA-transferase alpha (C; Keywords: COA-transferase; homodimer; Ketone body metabolism; mitochondrion (P; 1-39, Domain: transit peptide (mitochondrion) #status predicted <TNP>
                                                                                                                                                                                                                    A; Gene:
A; Map po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein VC1940 [imported] - Vibrio cholerae (group O1 C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18 - Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C;Accession: D82139
C;Accession: D82139
C;Accession: D82139
C;Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dc Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.;
C,R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-39/Domain: transit peptide (mitochondrion) **status predicted <TNP> F;38-274/Domain: 3-oxoadipate COA-transferase alpha chain homology <BAV F;40-520/Product: 3-oxoacid COA-transferase **status experimental <pre> CAATOR COA-Transferase **status experimental  CAATOR COA-Transferase beta chain homology <BAV F;302-506/Domain: 3-oxoadipate COA-transferase beta chain homology <BAV F;344/Active site: Glu **status predicted**
<u>В</u>
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                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: DNA Sequence of both chromosomes of the cholera A;Reference number: A82035; MUID:20406833 A;Accession: D82139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
D82139
                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-220 <HEI>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                A;Experimental
                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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Best Local S
Matches 6
                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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  176 VHFYTDSIN 184
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                                                  1 VTFYTDAVS
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6; Conser
                                                                                                                                                                                                                                                                                                source:
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                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                    GB:AE004269;
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100.0%; Pred. No. 87
Live 0; Mismatches
                                                                                                                         . 98;
                                                                                                                                                                                                                                                                                             GB:AE003852; NID:g9656466; Ol; strain N16961; biotype
                                                                                                  Ψ
                                                                                                                    Score 31;
Pred. No.
                                                                                                  Mismatches
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A:Map position: LG IIR
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                   A; Reference number: Z24398
A; Accession: T47218
                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, April 1996
A; Description: Isolation of the Neurospora cra
                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T47218
R; Sahni, M.; Kinsey, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [imported] - Neurospora
C;Species: Neurospora crassa
                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-338 <SAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;de Haan, L.A.M.; Willshaw, G.A.; van der Zeijst, B.A.M.; Gaastra, W. FEMS Microbiol. Lett. 83, 341-346, 1991
A;Title: The nucleotide sequence of a regulatory gene present on a pla A;Reference number: S20081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA A; Residues: 1-301 <DEH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surface virulence factor regulator - Escherichia coli C;Species: Escherichia coli
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A;Residues: I-256 <MTH>
A;Residues: I-256 <MTH>
A;Cross-references: GB:AE000854; GB:AE000666; NID:g2621839; PIDN:AAB85265.1; PID:g262185
A;Experimental source: strain Delta H
C:Genetics:
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                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Neurospora crassa
;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
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                                                         Query Match
Best Local
                                   Matches
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Best Local
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                                   Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 ITFFTDKV 168
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nes 5; Conser
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                                                 68.9%;
85.7%;
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62.5%;
                           Score 31; DB
Pred. No. 91;
0; Mismatches
                               0;
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Pred. No.
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91;
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                                                               Length 338;
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A;Cross-references: GB:L09703; NID:g304162; PIDN:AAC36838.1; PID:g30416 R;Daniel, R.A.; Errington, J. J. Gen. Microbiol. 139, 361-370, 1993 A;Title: DNA sequence of the murf-murD region of Bacillus subtilis 168. A;Reference number: A47691; MUID:93171879
                                                                                                                                                   A;Title: Cloning and sequencing of the cell division gene pbpB, which encodes penicil A;Reference number: A53292; MUID:94064553 A;Accession: D53292
                                                                                                         A; Molecule type: DNA
A; Residues: 1-69 < YAN>
                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                   R; Yanouri, A.; Daniel, R.A.; Errington, J. Bacteriol. 175, 7604-7616, 1993
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-589 <DAN>
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A;Molecule type: DNA
A;Residues: 1-553 <PAR>
A;Cross-references: GB:AL139078; GB:AL111168; NID:96968723; PIDN:CAB73804.1; PID:9696
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                       C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; B. Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter Jejuni reveals A;Reference number: A81250; MUID:20150912
A;Accession: F81282
                                                                                                                                                                                                                                                                                                                                                                                                   R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ferredoxin Cj1377c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C:Accession: F81282
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R;Daniel, R.A.; Drake, S.; Buchanan, C.E.;
J. Mol. Biol. 235, 209-220, 1994
A;Title: The Bacillus subtilis spoVD gene
A;Reference number: S43862; MUID:94118264
A;Accession: S43863 R;Errington, J. submitted to the EMBL Data Library, September 1993 A;Reference number: S49570 C;Species: Bacillus subtilis C;Date: 15-Mov-1996 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000 C;Accession: S49570; S43863; D53292; A47691; D69715; S23913 A;Status: preliminary; nucleic acid sequence not shown A;Cross-references: EMBL:225865; NID:g397893; PIDN:CAA81085.1; PID:g580936 R;Daniel, R.A.; Drake, S.; Buchanan, C.E.; Scholle, R.; Errington, J. penicillin-binding protein (spore cortex) spoVD - Bacillus subtilis N;Alternate names: stage V sporulation protein D preliminary 1-645 <ERR> encodes a mother-cell-specific penicillin-b

J.;

Buchanan,

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PIDN:AAC36838.1; PID:g304166

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A; Molecule type: DNA
A; Residues: 595-645 < CDA2>
A; Cross-references: EMBL:Z15056; NID:g40160; PIDN:CAA78766.1; PID:g40161
A; Cross-references: EMBL:Z15056; NID:g40160; PIDN:CAA78766.1; PID:g40161
A; Experimental source: strain 168
A; Note: sequence extracted from NCBI backbone (NCBIN:125659, NCBIP:125660)
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A; Note: sequence extracted from NCBI backbone (NCBIN:125659, NCBIP:125660)
A; Note: sequence of the Gram-position, G; Azevedo, V.; Berter
C.; Bron., S; Broulilet, S.; Brusche, B; Rose, M; Saddale, V.; Febrert, A.; Galler
A; Note: Sethelch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Lardinois, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serol akuchi, M.; Tamakoshi, A.; Tanakka, T.; Terpstra, P.; Tognoni, A.; Yata, V.; Uchiyama, T.; Minters, P.; Mipat, A.; Yamamotto, H.; Yamane, K.; Yasamotto, K.; Yata, K.; Yoshida, K.; A; A; Complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Natus: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
Search completed: June 13, 2001, 14:23:11 Job time: 742 sec
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A:Start codon: TTG
C:Superfamily: penicillin-binding protein 3
C:Keywords: membrane protein: sporulation
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A;Gene: spoVD
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A;Experimental source: strain 168
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| annotation update) annotation update) (ALPHA-AMYLASE/PULLULANASE) [INCLUDES | ed) | PRT; 1475 AA. | | ALIGNMENTS | | EL | | SPYA_MOUSE C | MDP1_SHEEP F | IT | | | ОСН | | SE | AP1_PIG F | |
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| JDES: | , | | | | arabidopsis | caenorhabdi | rattus norv | mus musculu | ovis aries | oryctolagus | sus scrofa | azotobacter | azotobacter | rattus norv | mus musculu | sus scrofa | |

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                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   MEDLINE-90147689; PubMed=2302196;
MEDLINE-90147689; PubMed=2302196;
Mathupala S.P., Saha B.C., Zeikus J.G.;
"Substrate competition and specificity at the active site of amylopullulanase from Clostridium thermobydrosulfuricum.";
Blochem. Blophys. Res. Commun. 166:126-132(1990).
Blochem. Blophys. Res. Commun. 166:126-132(1990).
-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-I- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULLULANASE PRECURSOR (ALPHA-MYLASE/PULLULANASE) [INCLUDES: ALPHA-AMYLASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE);
PULLULANASE (EC 3.2.1.41) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE);
(ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum)
Bacteria; Firmicutes; Bacillus/Clostridium group;
Thermoanaerobacter group; Thermoanaerobacter.
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, KNOWN AS THE ALPHA-AMYLASE FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                                                    PRINTS; PR00043; LEUZIPPRJUN. PROSITE; PS00036; BZIP_BASIC;
                                                                                                                                                                                                                                EMBL; L35273; AAA49537.1; HSSP; P05412; 1FOS.
                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95206115; PubMed-7898314;

Mastiuk K.L., Mello C.V., George J.M., Clayton D.F.;

"Immediate-early gene responses in the avian song control sy
cloning and expression analysis of the canary c-jun cDNA.";

Brain Res. Mol. Brain Res. 27:299-309(1994).

"FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND RECOGNIZE
ENHANCER DNA SEQUENCE: TGA(C/G)TCA.

"IS SUBUNIT: INTERACTS WITH C-FOS TO FORM A DIMER.

"IS SUBCELLULAR LOCATION: NICLEAR.
                                                                        Nuclear protein.
                                                                                                                                                                   Pfam; PF00170; bZIP; 1.
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Serinus canaria (Canary).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                        DNA_BIND
                                                                                               Proto-oncogene; Transcription
                                                                                                                                                                                    InterPro; IPR001871; -. InterPro; IPR002112; -.
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TRANSCRIPTION FACTOR AP-1 (PROTO-ONCOGENE C-JUN).
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SEQUENCE
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FIBRONECTIN TYPE-III.
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01-NOV-1997 (Rel. 3:
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Q29551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lk Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregor J., Davis N.W., Kirkpatrick H.A., Mau B., Shao Y.;
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lew H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burland
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RESULT
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Query Match
Best Local
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                              P43460;
01-NOV-1995
01-NOV-1995
30-MAY-2000
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
CSVR.
                                                                                                                     ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01144; COA_trans; 2.
PROSITE; PS01273; COA_TRANSF_1; 1.
PROSITE; PS01274; COA_TRANSF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rochet J.C., Bridger W.A.; "Identification of glutamate 344 as the catalytic residue active site of pig heart CoA transferase."; Protein Sci. 3:975-981(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Heart;
MEDLINE-92112838; PubMed-1730685;
                TRANSCRIPTIONAL
                                                                                                   CSVR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M80534; AAA31019.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94348427; PubMed=7915164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence of a transferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin T., Bridger W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.8.3.5) (SUCCINYL COA:3-OXOACID COA-TRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVE SITE
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                                                                                                                                                                                          42 FYTDAV
                                                                                                                                                                                                                          3 FYTDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: MITOCHONDRIAL. SIMILARITY: TO OTHER CO-TRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY:
A 3-OXO-ACYL-COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: KEY ENZYME FOR KETONE BODY CATABOLISM. TRANSFERS THE MOIETY FROM SUCCINATE TO ACETOACETATE. FORMATION OF THE ENZYME INTERNEDIATE PROCEEDS VIA AN UNSTABLE ANHYDRIDE SPECIES FORMED BETWEEN THE CARBOXYLATE GROUPS OF THE ENZYME AND SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR001618; -. PF01144; CoA_trans;
                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem.
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520
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267:975-978(1992).
              1. 32, Created)
1. 32, Last sequence up
1. 39, Last annotation
ACTIVATOR CSVR.
                                                                                                   STANDARD;
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344
56407
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520
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                                                                                                                                                                                                                                                                         71.1%;
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                                                                                                                                                                                                                                                                           Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              Transit peptide.
MITOCHONDRION.
SUCCINYL-COA:3-KETOACID-COENZYME
TRANSFERASE.
COA-BINDING (POTENTIAL).
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                                update)
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                                                                                                                                                                                                                                                                             DB 43;
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ina; Suidae;
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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RESULT 7
G3P_NEUGE
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Best Local S
Matches 5
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P54118; Q92255;
01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interrity

Pfam: pF00165; HTH_ALGE,

Pfam: pF00165; HTH_ARAC.

PRINTS; PR00032; HTH_ARAC_FAMILY_1; 1.

PROSITE: PS01041; HTH_ARAC_FAMILY_2; 1.

PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.

PROSITE: PS01124; HTH_ARAC_FAMILY_1; 1.

PROSITE: PS01124; HTM_ARAC_FAMILY_1; 1.

PROSITE: PS01124
Dunlap J.C., Shinohara M.L., Bell-Pedersen D., Loros Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databas -- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + NADH(+) -- 1.3-DIPHOSPHATEGLYCERATE + NADH, -- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOI-I- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Sahni M., Kinsey J.A.;
Sahni M., Kinsey J.A.;
"Identification and cloning of the Neurospora phosphate dehydrogenase gene, gpd-1.";
Fungal Genet. Newsl. 44:47-49(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizom
Sordariales; Sordariaceae; Neurospora
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPD-1 OR CCG-7
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STRAIN-E10703 / SEROTYPE
MEDLINE-92120486; PubMed-
de Haan L.A., Willshaw G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haan L.A., Wilshaw G.A., van der Zeijst B.A., Gaastra W., he nucleotide sequence of a regulatory gene present on a plenterotoxigenic Escherichia coli strain of serotype 0167:H MS Microbiol, Lett. 67:341-346(1991).

FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE FIMBRIAL GENE ENTEROTOXIGENIC ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
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PubMed=1685133;
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62
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No.
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                                            GLYCOLYSIS
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serotype 0167:H5.";
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                                                                                                                                                                                                                                                                                                                                                              glyceraldehyde-3-
                                                                                                               ORTHOPHOSPHATE
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RESULT
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Best Local s
Matches 6
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SP5D_BACSU STANDA

003524;

01-OCT-1993 (Rel. 27,

01-OCT-1994 (Rel. 30,

01-OCT-1996 (Rel. 34,

STAGE V SPORULATION F

BINDING PROTEIN).
                                                                                                                                    MEDLINE=94118264; PubMed=8289242; Daniel R.A., Drake S., Buchanan C.E., Scholle R., Errington J.; "The Bacillus subtilis spovD gene encodes a mother-cell-specific penicillin-binding protein required for spore morphogenesis."; J. Mol. Biol. 235:209-220(1994).
                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO
Glycolysis;
 Daniel
                     SEQUENCE OF STRAIN=168;
                                                 "Cloning and sequencing of the cell penicillin-binding protein 2B in Bac J. Bacteriol. 175:7604-7616(1993).
                                                                                 MEDLINE=94064553; PubMed=8244929; Yanouri A., Daniel R.A., Erringto
          MEDLINE=93171879;
                                                                                                           STRAIN=168;
                                                                                                                                                                                                                                                                          SPOVD
                                                                                                                      SEQUENCE OF
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000173; -. Pfam; PF00044; gpdh; 1. PRINTS; PR00078; G3PDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U56397; AAB00570.
EMBL; U67457; AAB95425.
HSSP; P00357; 1GPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                           1 VTFYTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                       VKFYTDA
R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
338
                               595-645 FROM N.A.
                                                                                                                     1-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        79
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212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                    FROM
         PubMed=8436954;
                                                                                                                                                                                                                                                                                           27, Create
30, Last s
34, Last a
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212
36193
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                                                                                                                    N.A.
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83
                                                                                                                                                                                                                                                 Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                      group;
                                                           Errington J., Buchanan C.E of the cell division gene pin 2B in Bacillus subtilis.
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THE GLYCERALDEHYDE
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(BY SIMILARITY).
ACTIVATES THIOL GROUP DURING
(BY SIMILARITY).
DA -> ER (IN REF. 2).
A -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                         notation update)
(SPORULATION SPECIFIC
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                       Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> ER (IN REF. 2)
-> S (IN REF. 2)
62C8F5896D3B2F57
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                               645
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB . 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                               pbpB,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                          PENICILLIN-
                                                                       which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYSIS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 225865; CAA81085 1; -
EMBL; L09703; AAC36838 1; -
EMBL; 215056; CAA78766 1; -
EMBL; 268230; CAA92528 1; -
EMBL; 259111; CAB13390 1; -
EMBL; 23913; S23913.
PIR; S23913; PIR; A47691; A47691
                                                                                                                                                                                                                                                                                                                             ONKEP1;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE
(EC 2.1.1.14) (METHIONINE SYNTHASE).
                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restructed the European Bioinformatics Institute.
                                                                                                                                                                                                                                           Bacillus halodurans.
Bacteria; Firmicutes; Be
Bacillus/Staphylococcus
Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACHD
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Pfam; PF00905; Transpeptidase; 1.

Peptidoglycan synthesis; Cell wall;

SEQUENCE 645 AA; 71261 MW; OAODE
  "Complete genome sequence of the alkaliphilic bacterium halodurans and genomic sequence comparison with Bacillus Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                Takami H., Nakasone K., Takaki Y., Maeno G., S
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-168;
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                                                                              Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KFP1;
01-OCT-2000
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TISSUE SPECIFICITY: FOUND ONLY IN MOTHER CELLS.
DEVELOPMENTAL STAGE: EXPRESSED DURING SPORULATION.
SIMILARITY: TO VARIOUS OTHER PENICILLIN-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
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6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the murE-murD region of Bacillus subtilis 168."; biol. 139:361-370(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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87
                                                                                                                                                                                                                                                                       Bacillus/Clostridium group;
us group; Bacillus.
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                                                                                                                                                                                                                                                                     group;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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0A0D8966B6D0C2F4 CRC64;
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                                                                                                  Sasaki R.
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                                                                                           R.,
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                                                  Bacillus
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                           subtilis
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RESULT
NID2_H
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                          NID2_HUMAN STANDARD; PRT; 13/5 AA. Q14112; 043710; 15-DEC-1998 (Rel. 37, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) NIDOGEN-2 PRECURSOR (NID-2) (OSTEONIDOGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NIDO....
Homo sapiens (Human).
Homo sapiens (Human).
Charia; Metazoa; Chordata;
Charia; Primates;
                      Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: CELL ADHESION GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN BASEMENT MEMBRANES. BINDS TO COLLAGENS I AND IV, TO PERLECAN AND TO LAMININ 1. DOES NOT BIND FIBULINS. IT PROBABLY HAS A ROLE
                                                                                                                                                                protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase;
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                                                                                                         Ohno I.,
                                                                                                                                                                                           Ohno I., Hashimoto J.,
                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Cancellous bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                              'Human osteonidogen localization.";
                                                                                                           SEQUENCE FROM N.A. Ohno I., Okubo K.,
                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                           properties.";
                                                                                                                                                                                                                                                                         Nidogen-2: a new basement membrane
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=98406162; PubMed=9733643;
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                 MOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VTFYTDAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMOCYSTEINE - TETRAHYDROPTEROYLTRI L-GLUTAMATE + L-METHIONINE.
COFACTOR: ZINC; BINDS ONE MOLE PER SUBUNIT (BY SIMILARITY).
PATHWAY: TERMINAL STEP IN THE DE NOVO BIOSYNTHESIS OF METHIONINE.
SIMILARITY: BELONGS TO THE VITAMIN-B12 INDEPENDENT METHIONINE
IN CELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORMATION (BY SIMILARITY).

CATALYTIC ACTIVITY: 5-METHYLTETRAHYDROPTEROYLTRI-L-GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CATALYZES THE TRANSFER OF A METHYL GROUP FROM METHYLTETRAHYDROFOLATE TO HOMOCYSTEINE RESULTING IN METH
                                                                                                                                                   cloning and characterization (ein: osteonidogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTFYEEVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP001508; BAB04157.1; -.
           CELL-EXTRACELLULAR MATRIX INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
6; Conserv
                                                                                                                                                 (JUL-1996) to
SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             639
641
724
756 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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639 639 ZINC (BY SIMILARITY).
641 ZINC (BY SIMILARITY).
724 724 ZINC (BY SIMILARITY).
56 AA; 85156 MW; 6F7FA9352A42AE6A CRC64;
                                                                                                                                                                                                                                                 282:99-109(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251
                                                                                                           Matsubara
                                                                                            gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.9%;
66.7%;
                                                                                                                                                                                                                                                                                         Goehring W.,
                                                                                           .intron-exon
                                                                                                                                                   EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                           <u>~</u>
                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                           of a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
NO.
                                                                                                                                                                                                                                                                                                                    N-TERMINUS
                                                                                                                                                                                                                                                                           protein with
                                                                                                                                                                                                                                                                                         Timpl R.;
                                                                                            junctions
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1e+02;
AND
                                                                                                                                                                              Okubo K., Matsubara K.; for the novel bone matr
                                                                                                                                                   databases
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                                                                                              and chromosomal
                                                                                                                                                                                                                                                                            diverse binding
LESS
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H
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PANCREAS,
                                                                                                                                                                               bone matrix
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Calcium-binding; F
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SIGNAL 31
CHAIN 484
DOMAIN 759
DOMAIN 801
DOMAIN 892
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DISULFID 763
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DISULFID 805
                                                                                                                                                                                                                                                                                                                                          InterPro: IPR00003; ...
InterPro: IPR000152; ...
InterPro: IPR000152; ...
InterPro: IPR000561; ...
InterPro: IPR000716; ...
InterPro: IPR000716; ...
InterPro: IPR00078; EGF; 5.
Pfam: PF00008; EGF; 5.
Pfam: PF00086; thyroglobulin_1; 2.
Pfam: PF00086; thyroglobulin_1; 2.
PROSITE: PS00048; THYROGLOBULIN_1; 2.
PROSITE: PS00186; EGF_2; 4.
PROSITE: PS01186; EGF_2; 4.
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PTM: HIGHLY
SIMILARITY:
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AB009799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
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Z N- AND O-GLYCOSYLATED.

CHOMTAINS 5 EGF-LIKE DOMAINS.

CONTAINS 2 THYROGLOBULIN TYPE-I DOMAINS.

CONTAINS 5 LDL-RECEPTOR YWTD DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAA24112.1
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11200
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113288
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11373
7766
7866
8427
                                                                                                                                                                                                                                                                                                                 Extracellular matrix; epeat; EGF-like domain
EGF-LIKE 1.
EGF-LIKE 3, CALCIUM-BINDING (1)
EGF-LIKE 3, CALCIUM-BINDING (1)
EGF-LIKE 5, CALCIUM-BINDING (1)
EGF-LIKE 5, CALCIUM-BINDING (1)
THYROGLOBULIN TYPE I 1.
THYROGLOBULIN TYPE I 2.
LDL-RECEPTOR YWTD MOTIF 1.
LDL-RECEPTOR YWTD MOTIF 3.
LDL-RECEPTOR YWTD MOTIF 3.
LDL-RECEPTOR YWTD MOTIF 4.
LDL-RECEPTOR TYPE MOTIF 5.
BY SIMILARITY.
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; Cell adhesion.
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IDH2_YEAST
P28241;
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CARBOHYD
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01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
ISOCITRATE DEHYDROGENASE (NAD) SUBUNIT 2, MITOCHONDRIAL
(EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC I
DH2 OR YOR136W OR O3326 OR YOR3326W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces.
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
SEQUENCE
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CARBOHYD
CONFLICT
                                                                                    Voss H., Benes V., Andrade M.A., Valencia A. Schwager C., Paces V., Sander C., Ansorge W "DNA sequencing and analysis of 130 kb from yeast 13:655-672(1997).
                                                                                                                                                                                                                                                                                                        STRAIN=S288C / FY1679;
MEDLINE=97060020; PubMed=8904341;
MEDLINE=97060020; PubMed=8904341;
Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vlcek C.,
Wiemann J., Zimmermann J., Erfle H., Paces V., Ansorge W.;
"Stegemann J., Zimmermann J., Erfle H., Paces V., Ansorge W.;
"Stegemann J., Zimmermann J., Erfle H., Paces V., Ansorge W.;
"Sequencing and analysis of 51 kb on the right arm of chromosome X
"Sequencing and analysis of 51 kb on the right arm of chromosome X
"Sequencing and analysis of 51 kb on the right arm of chromosome X
"Sequencing and Strange C., Vlcek C.,
Vlcek C.,
"Sequencing and Strange C., Vlcek C., Vlcek C.,
"Sequencing and Strange C., Vlcek C., Vl
SEQUENCE OF STRAIN-SG7;
                                                                                                                                                                                  MEDLINE=97344368; Pubmed=9200815; Voss H., Benes V., Andrade M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1222 VLFYTDLVN 1230
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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N-LINKED (GLCNAC. . .) (PROBABLE).

ON (IN REF. 3).

G -> W (IN REF. 3).

ESSAVVKLANPLHFVEARFSULYVGTNGIISTQDFPRETQY

VDYDFPTDFPAIAPFLADIDTSHGRGRVLYREDTSPAVLGL

AARTVRAGFFRSARFTFTHAFLATWEQVGAYETKRE

VKLSRGSAGESPALTKPDSARTSTRATAEAESCTERTFPPQCWA

WFPAMCALASRALRAFYPHPRLPGHLGAGRRLRGGQTR

WPPAMCALASRALRAFYPHPRLPGHLGAGRRLRGGQTR
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Pred. No. 1.9e
1; Mismatches
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D -> G (IN REF. 1).
W; 414299D244205FBC
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1.9e+02;
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                                                                                                                                                                               Rechmann
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Best Local Similarity
Matches 6; Conserv
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EMBL; X94335; CAA64054.1; -.
EMBL; Z75043; CAA69335.1; -.
EMBL; X90518; CAA62110.1; -.
PIR; A39309; A39309.
HSSP; P00351; 1051.
SGD; S0005662; IDH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PFOULDY; Lawrin, Prosite; PSO0470; IDH_IMH; 1.

PROSITE; PSO0470; IDH_IMH; 1.

Oxidoreductase; NAD; Tricarboxylic acid cycle; Transit peptide;

Mitochondrion; Allosteric enzyme; RNA-binding.

MITOCHONDRION.

TRANSIT 1 15 MITOCHONDRION.

CHAIN 16 369 ISOCITRATE DEHYDROGENASE (NAD) SUBUNIT 2.

CHAIN 113 BINDING TO ISOCITRATE (BY SIMILARITY).

CONFLICT 25 25 R -> G (IN REF. 4).

CONFLICT 26 AA: 39739 MW; 3A48C999776CE373 CRC64;
                                                                          YL90_MYCTU STANDARD; PRT; 3
Q10383; O53524;
Q1-OCT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
HYPOTHETICAL 39.8 KDA PROTEIN RV2190C.
RV2190C OR MTCY190.01C OR MTV021.23C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keys D.A., McAlister-Henn L.;
"Subunit structure, expression, and function of NAD(H)-specific isocitrate dehydrogenase in Saccharomyces cerevisiae.";
J. Bacteriol. 172:4280-4287(1990).
                                                                                                                                                                                                                                                                                               MYCTU
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MEDLINE-94089379; PubMed-7505425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001804; -. Pfam; PF00180; 1sodh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grivell L.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90330530; PubMed-2198251;
                                                                                                                                                                                                                                                                                                                                                                                                              250
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||||||
250 YTDAVS 25
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SUBUNIT: OCTAMER OF TWO NONIDENTICAL SUBUNITS IDH1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CO(2) + NADH.
ENZYME REGULATION: ALLOSTERICALLY REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: MITOCHONDRIAL.
SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEHYDROGENASES FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
  Corynebactérineae;
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100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                 385
                                                                                                                                            update)
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Best Local
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079436;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holroyy Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyy L., Oliver S., Osborne J., Ouall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                 entities re
or send an
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3). MTND4 OR ND4 OR NADH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as as its content is in modified and the content in the content in the content is in the content in the con
                                                                                                                                                                                                                                                                                                                                              GENOMICS 50:161-169(1998).
-I- CATALYTIC ACTIVITY: NADH + UBIQUINONE =
                                                                                                                                                                                                                                                                                                                                                                                                                                      cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98317530; PubMed-9653643;
Gissi C., Gullberg A., Arnason U.;
"The complete mitochondrial DNA sequence of the rabbit, Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9986;
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                                 to license@isb-sib.ch).
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RESULT
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Best Local :
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InterPro; IPR00250;
InterPro; IPR001750; -
Pfam; PF00361.
                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9XSB5; O9TTS2;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ESTROGEN RECEPTOR BETA (ER-BETA).
                                                                                                                                                                                                                                                                                                                      Walther N., Lioutas C., Tillmann G., Ivell R.;

"Cloning of bovine estrogen receptor beta (Erbeta): expression of novel deleted isoforms in reproductive tissues.";

MO1. Cell. Endocrinol. 152:37-45(1999).

-!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANUER.

MAY PLAY A ROLE IN OVARIAN FOLLICULAR GROWTH AND MATURATION.

-!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, sequencing, and localization of bovine estrogen receptorbeta within the ovarian follicle."; Biol. Reprod. 60:691-697(1999).
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Pfam; PF01059; oxidored_q5.N; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 459 AA; 51599 MW; 11B5ACA972DD97E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-HOLSTEIN; TISSUE-Ovarian follicle;
MEDLINE-99150196; PubMed-10026117;
Rosenfeld C.S., Yuan X., Manikkam M., Calder M.D., Garverick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVIN
                            EMBL; AF110402; AAD24432.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99359179; PubMed-10432221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 4-527 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lubahn D.B.;
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Bovidae; Bovinae; Bos.
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| 55 TFFSDALS 62
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nes 5; Conserv
                                                                                                                                                                                                                                                                      ALPHA (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: PRESENT IN GRANULOSA CELLS
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                                                                                                                                                                                                          IN VARIOUS STAGES OF FOLLICULAR GROWTH.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DUA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                              NR3 SUBFAMILY.
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               Y18017;
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             CAB53861.1; ALT_INIT
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Cetartiodactyla;
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62.5%;
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Pred. No.
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                                                                           (See http://www.isb-sib.ch/announce/
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RESULT 15
ESR2_SHEEP
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Best Local
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Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00347; STROIDFINGER.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00346; THYROIDHORMR.
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09TU15; Q9NOT6;
01-OCT-2000 (Rel
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InterPro; IPRO00536; -.
InterPro; IPRO01628; -.
InterPro; IPRO01723; -.
InterPro; IPRO01728; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
MOD_RES
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                       -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
-!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH EF
                                                                                                                                                                                                                                                                                                                                                                            ovary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
Bovidae; Caprinae; (
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESR2 OR NR3A2.
Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (Rel. 40, I
01-OCT-2000 (Rel. 40, I
ESTROGEN RECEPTOR BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; 9300031, NUCLEAR_RECEPTOR; 1.

Receptor; Transcription regulation; DNA-bindir
Zinc-finger; Steroid-binding; Phosphorylation.
DOMAIN 1 145 MODULATING.
                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                Cardenas H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                "Cloning
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                                                                                                                                  ALPHA (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR.

ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; BETA (SHOWN HERE)

BETA-1; ARE PRODUCED BY ALTERNATIVE SPLICING.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DO

A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                      NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              and expression
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(Rel. 40, Last seq
(Rel. 40, Last ann
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146
182
212
212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Chordata; Craniata; Vertebrata; Euteleostomi;
; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISOFORMS
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211
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C4-TYPE.
C4-TYPE.
STEROID-BINDING.
PHOSPHORYLATION (BY SIN
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Pred. No.
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N -> D (IN REF.
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SIMILARITY).
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CC or send an email to licensed&ib-sib.ch).

CR EMBL, AP17795; AAD5772.1; ...

DR EMBL, AP257109; AAF71745.1; ...

DR HISSP, P03772; HRCD.

DR InterPro; IPR000324; ...

DR InterPro; IPR000324; ...

DR InterPro; IPR000324; ...

DR InterPro; IPR000324; ...

DR Pfam: PF00104; hormone_rec; 1.

DR Pfam: PF00104; bromone_rec; 1.

DR Pfam: PF00104; bromo
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Title:
Perfect score:
Sequence:
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Maximum
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length: 2000000000
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Match
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1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
June 13, 2001, 14:29:43; Search time 150.43 Seconds (without alignments) 7.012 Million cell updates/sec
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Gapop 10.0 ,
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sp_phage:*
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sp_bacteria:*
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      Q9x5n2 myxococcus
Q9m2n3 arabidopsis
Q75728 homo sapien
Q9pvz1 xenopus lae
Q9pvz0 xenopus lae
Q9zs99 arabidopsis
Q9m100 arabidopsis
Q98159 little cher
                                                                                                                    09x7n2 bacillus ha
09s3x7 streptomyce
09sbx7 bacillus ha
09x6t5 streptomyce
094831 homo sapien
09vkb9 drosophila
                                                                               065728 cicer ariet
Q9v2z4 methanosarc
Q9v010 pyrococcus
P91538 caenorhabdi
                                                                                                                                                                                   Description
                                                                                RESULT
Q9S3X7
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                              Q9S3X7
Q9S3X7;
                          SPCC (FRAGMENT).
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| Q9K7N2; 01-OCT-2000 01-OCT-2000 01-OCT-2000 | 7N2 Q9K7N2 | OLT 1 | | ωu | . w | 2 3 | υ , | v س | ວໝ | 7 | 6 3 | 5 | 3 | ω i | ω t | 31 31 | 9 | 8 3 | 7 3 | 6 | 5 | 4 ω | ω ω | 2 | 21 31 | 0 3 | |
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| (TrEMBLrel (TrEMBLrel | PRELIMINARY; | | | 66.7 | . 0 | 6. | 6 : | 20 00 | 66.7 | 6 | 5 | ٥. | <u>σ</u> | 9 | ∞: | æα | | 8 | 8 | 8 | 8 | œ | œ • | œ | 8 | ω. | |
| | INARY; | | | 387 | 356 | 348 | 337 | 286 | 255 | 240 | 216 | 188 | 176 | 73 | 3620 | 2247 | 879 | 879 | 756 | 693 | 690 | 649 | 553 | 418 | 263 | 256 | |
| 15, 15, 15, | | | | 2 | 1 | 10 | σı | , r | ง | 10 | 2 | u | N | 9 | σ, | ۲ ا | N | 2 | N | 5 | N | N | N | N | N | 1 | |
| Created) Last seq Last ann | PRT; | · | ALIGNMENTS | 025008 | Q9QZK9 | Q9LKS2 | Q9VB91 | 092CX1 | 006932 | Q9SN71 | Q9RV40 | Q22169 | 054024 | 048462 | 09TU53 | 031480 | 031504 | 030579 | Q9KFP1 | Q9V7K0 | Q9S307 | P73736 | Q9PMS3 | Q9Z5R3 | Q9KZK4 | 026856 | |
| ed) sequence update) annotation update) | 260 AA. | | MENTS | | | | | | | | | | | | | | | | | | | | | | | | |
| | • | | | 025008 helicobacte | 09qzk9 rattus norv | Q91ks2 arabidopsis | | 09zcx1 rickettsia | | \vdash | 0 deinococcu | | | ioph | | Q91u53 arabidopsis | , ה | bacillus | | _ | ruminococc | 6 synechocys | | 0 | kzk4 streptomyc | 026856 methanobact | |

OC GREET DE AC 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) SEQUENCE FROM N.A. STRAIN-C-125 / JCM 9153; STRAIN-C-125 / JCM 9153; STRAIN-C-125 / JCM 9153; STRAIN-C-126 / JCM 9153; Bacillus halodurans. Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID-86665; MOLYBDENUM TRANSPORT SYSTEM (MOLYBDATE-BINDING PROTEIN). BH3329. Streptomyces spectabilis. Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; 80.0%; 2; Score 36; I Mismatches 98 DB 2; 8.1; ₹ Length 260; Indels 0, Gaps

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RESULT
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AC 05
AC 0
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Matches 6
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Altenbuchner J., Jennen D., Volff J.,
Altenbuchner J., Jennen D., Volff J.,
The spectinomycin resistance gene o.
Streptomyces spectabilis.";
Submitted (JUL-1999) to the EMBL/Genl
EMBL, AR170704; AAD50451.1;
INTERPRO, IPR000954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrE
01-0CT-2000 (TrE
01-0CT-2000 (TrE
BH1883 PROTEIN.
                                                                                                                Streptomyces spectabilis.
Bacteria; Firmicutes; Actinobacter
Actinomycetales; Streptomycineae;
NCBI_TaxID=68270;
                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2000 (TrEMBLrel. 15,
      Hyun
                       SEQUENCE FROM N.A.
STRAIN-ATCC27741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001513; BAB05602.1; .
SEQUENCE 365 AA; 39312 MW; 69DF161C75A57692 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Q9X6T5;
                                                                                                                                                                                                                                                              SPCS1
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Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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NCBI_TaxID=68270;
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les 6; Conserv
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   Kim
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BCDNA:LD23336 PROTEIN.
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJINE-99087487; PubMed-9872452;
MEDIJINE-99087487; Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which co for large proteins in vitro.";
DNA Res. 5:277-286(1998).
EMBL; ABO18269; BAA34446.1; -.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF145039; AAD18489.1; -.
HSSP; P04181; 2CAN.
INTERPRO; IPR000954; -.
PFAM; PF00202; aminotran_3; 1.
PROSITE: PS00600; AA_TRANSFER_CLASS_3; UNKNOWN_1.
Transferase: Aminotransferase.
SEQUENCE 442 AA; 47574 MW; B2165F082EA4BBZE CRC64;
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[1] SEQUENCE FROM N.A.

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MEDLINE-20196006; PubMed-10731132;

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Pleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rahert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Milliams S.M., Moy M., Murphy B.,
RA Williams S.M., Woy M., Weissenbach J.,
RA Yelos R.A., Werse E. M., Rubhila M., Shou M., Shang G., Zhao Q., Zheng L.,
RA Chang R., Sun E.,
RA Chang R., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Myers E. M., Ra, Raharis M., Shing G., Zhao Q., Zheng L.,
RA Chang R., Shing R., Werter J.C., Shink H.O.,
RA Chang R., Shink H., Shink H., Shink H., Shink H.O.,
RA Chang R., Shink H., 
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                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                            "Full length Drosophila melanogaster cDNA sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databbases.
-I- ALTERNATIVE PRODUCTS: THREE ISOFORM; ISOFORM 1 (SHOW
ISOFORM 2 AND ISOFORM 3; ARE PRODUCED BY ALTERNATIVE
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                                                                                                                       SEQUENCE
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AE003634; AAF53157.1;
AE003634; -; NOT_ANNOTATED_CDS.
AF145682; AAD38657.1;
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               Mismatches
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Best Local
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF178830; AAD51814.1; ...
SEQUENCE 472 AA; 52671 MW; C818616BB5C30A58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TEEMBLrel. 13, Created)
01-MAY-2000 (TEEMBLrel. 13, Last sequence update)
01-MAY-2000 (TEEMBLrel. 13, Last annotation updat
ACETYL-COA DECARBONYLASE/SYNTHASE BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. CASTELLANA; TISSU Labrador E., Esteban R., Dop Submitted (MAR-1998) to the EMBL; AJ004959; CAA66244.1; INTERPRO; IPRO02422; -.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Cicer.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 16.9 KDA PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                      Sencic S., Grahame D.A.;
"Structure and function of acetyl-CoA decarbonylase/synthase (ACDS)
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mes 6; Conserv
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                                                                                                                         Score 33;
Pred. No.
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Best Local S
Matches 6
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Latster N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
EMBL;
                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
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01-MAY-1997
01-JUN-2000
                                 Waterston R.;
Submitted (DE
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Wamsley P., Kramer
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Q9V0I0;
01-MAY-2000 (3
01-MAY-2000 (7
01-JUN-2000 (7
HYPOTHETICAL (9
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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structure and evolution.";
Submitted (JUL-1999) to the
EMBL; AJ248285; CAB49723.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COSMID ZC204.
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Archaea; Euryarchaeota; Thermococcales;
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tted (DEC-1996) to the U80839; AAB37917.1; -.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
L 52.6 KDA PROTEIN.
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                EMBL/GenBank/DDBJ databases.
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SQ
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L Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL, AF127082; AAD31004.1; -.
R INTERPRO; IPR001375; -.
R INTERPRO; IPR001375; -.
R INTERPRO; IPR002470; -.
R INTERPRO; IPR002471; -.
R INTERPRO; IPR002471; -.
R PFAM; PF00326; Peptidase_S9; 1.
R PFAM; PF00326; PRO_ENDOPEP_SER; 1.
R PRINTS; PR00862; PRO_ENDOPEP_SER; 1.
SEQUENCE 689 AA; 76847 MW; 474FB9BB957D6DCB CRC64;
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Best Local S
Matches 6
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Best Local :
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Q9M2N3;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2000
 Submitted [2]
                    Salanoubat M.
                          Nyakatura G., Fartma
Weichselgartner M.,
                                                                      Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
                                            SEQUENCE FROM
                                                                                                                  T27B3.60.
                                                                                                                          HYPOTHETICAL
                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Pro
Myxococcales;
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01-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=34;
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nes 6; Conserv
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O (Tremblrel. 15,
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AL 74.7 KDA PROTEI
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                                     Fartmann
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                          ann B.,
Mewes !
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85.7%;
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H.W., Le
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Last annotation update)
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Myxococcaceae; Myxococcus.
                                    D.,
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                                   Sterr W.,
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                        r W., Holland
Mayer K.F.X.,
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SEQUENCE FROM N.A. EU Arabidopsis seq

EU Arabidopsis sequencing project; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL137079; CAB68120.1; -. Hypothetical protein. SEQUENCE 695 AA; 74673 MW; C720E0ED69B41E98 CRC64;

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Q9PVZ1;
Q1-MAY-2000
Q1-MAY-2000
Q1-CCT-2000
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NON_TER
SEQUENCE
                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
Amphiba; Batrachia; Anura; Mesobatrachi
Xenopodinae; Xenopus.
MCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human IgA and IgM secreting intestinal plasma cells carry mutated VH region genes.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009525; CAA08732.1; -.
INTERPRO; IPR003006; -.
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Schuler-Metz A., Knoechel S., Knoechel W.; "Xvent-2 and c-Jun (AP-1) mediate auto-cat expression in Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata;
Theria; Primates;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       C-JUN PROTEIN.
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75.08;
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Mesobatrachia; Pipoidea;
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                              expression in Xenopus embryos.";
Submitted (JUL-1999) to the EMBL/C
EMBL; AJ243955; CAB51637.1; -
HSSP; PD6412; IPOS.
INTERPRO; IPR001871; -
INTERPRO; IPR002112; -
INTERPRO; IPR002112; -
PFAM; PF00170; bZIP; 1.
PRINTS; PR00043; LEUZIPPRJUN.
PROSITE; PS00036; BZIP_BASIC; 1.
SEQUENCE 314 AA; 34556 MM; 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ243954; CAB51636.1; -.
HSSP; P05412; 1FOS.
INTERPRO; IPRO01971; -.
INTERPRO; IPRO02112; -.
PFAM; PF00170; bZIP; 1.
PRINTS; PRO0043; LEUZIPPRJUN.
PROSITE; PS00036; BZIP_BASIC; 1.
SEQUENCE 312 AA; 34363 MW; 3B99698703A4E3E1 CRC64;
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la; Pipoidea; Pipidae;
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Listing first 45 summaries
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US-09-184-658-48
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US-07-671-817A-5
US-07-671-817A-6
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Patent No. 5945510
GENERAL INFORMATION:
APPLICANT: FASANO, Alessio
TITLE OF INVENTION: BYSTANTIALLY
TITLE OF INVENTION: PHYSIOLOGICAL
TITLE OF INVENTION: MAMMALIAN TIC
                                                                                                                                                                                                                                                                       TELEFAX: (202) 293-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7660
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: KIT, Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2100 Pennsy CITY: Washington, E STATE: D.C. COUNTRY: U.S.A.
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TYPE: an
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US-09-053-549-6
PCT-US95-05431-19
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US-08-754-490-10
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US-08-983-607-22
; Sequence 22, Application US/08983607
; Patent No. 6140470
; Patent No. 6140470
                 RESULT 3
US-09-038-909-2
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US-08-983-607-22
Sequence 2, Application US/09038909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 119 residues
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fUSE5 fusion phage construct
CLONE: G57
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CTASCIFICATION: A18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS DOS
SOFTWARE: WORD PROCESSING
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERAL INFORMALIANT AND GAIEN APPLICANT: Alan Garen APPLICANT: Xiaohong Cai TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-TITLE OF INVENTION: bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 203-773-9544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.
                                                                                         58 TYYTDSV 64
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
                                                                                                                              2 TFYTDAV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Department of Molecular Biophysics ADDRESSEE: and Biochemistry, Yale University STREET: 266 Whitney Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New Haven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Connecticut RY: United States of America 06520-8114
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Mary M. Wilmber: 32423
                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                   68.98;
71.48;
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                                                                                                                                                                                 Score 31; DB 4; Length 119; Pred. No. 46;
                                                                                                                                                                   Mismatches
                                                                                                                                                               Indels
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Query Match
Best Local Similarity
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           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 116
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence 48, Application US/09184658 Patent No. 6030792
                                                              APPLICANT: Downs, James T.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Protein Fragments
FILE REFERENCE: PC9946-A
CURRENT EPPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER FILING DATE: 1998-11-02
EARLIER APPLICATION UMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6083924
GENERAL INFORMATION:
                                                                                                                                                                                                                                         APPLICANT: Mezes, Peter S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                           APPLICANT: Otterness,
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/038,909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     102 VQYYTDIVS 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 466 amino TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                        1 VTFYTDAVS 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 19103-2793
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Earnshaw, David
McDevitt, Damien
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EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
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, NAME/KEY: DOMAIN
; LOCATION: (1)..(116)
; OTHER INFORMATION: Mature 5109 VH.
US-09-184-658-48
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Best Local Similarity
"Thes 5; Conserve
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Query Match
Best Local Similarity b2...
Conservative
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                                                                                                         NAME/KEY: SITE
LOCATION: (284)...(289)
OTHER INFORMATION: H15 tag.
-09-184-658-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SIGNAL LOCATION: (1)..(22) OTHER INFORMATION: p. OTHER INFORMATION: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Assays for Measurement of Protein Fragments in TITLE OF INVENTION: Biological Media FILE REFERENCE: PC9946-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Otterness, Ivan G.
APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: scfv.
                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (270)..(279)
OTHER_INFORMATION: myc tag.
                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (155)..(266)
OTHER INFORMATION: 5109 VL domain.
                                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (139)..(154)
OTHER INFORMATION: 16 amino acid linker.
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LOCATION: (23)..(138)
OTHER INFORMATION: 5109 VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                      Score 30; DB 3; Le
Pred. No. 1.7e+02;
2; Mismatches 1;
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Pred. No.
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                                                     Length 289;
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                        Indels
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Best Local Similarity
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PCT-US93-05000-6
                                                                                                                                                                                         ;Patent No. 5523211
, APPLICANT: PUSZTAI-CAREY, MARIANNE;CAREY, PAUL R.; LESSARD, TIMOTHY;YAGUCHI, MAKOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US93-05000-6
                                                                                                                                                                                                                                                5523211-2
                                                                                                                                                        ; TITLE OF INVENTION: IDENTIFICATION, QUANTITATION AND ;PURIFICATION OF INSECTICIDAL PROTEINS FROM BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application PC/TUS9305000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 05
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: D-
NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                APPLICATION NUMBER: US/
FILING DATE: 19-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                     NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 26-MAY-1992.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
                                                                                                                                                                                                                                                                                                                    127 YTDAVS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
APPLICATION NUMBER: 102,491
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: 836,967
FILING DATE: 19-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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DGY: unknown
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                                                                                                        US/08/277,076
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hes 0;
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Best Local Similarity 71.45.
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PUSZTAI-CAREY, MARIANNE; CAREY, PAUL R.; LESSARD, TIMOTHY; YAGUCHI, MAKOTO IDENTIFICATION, QUANTITATION AND INSECTICIDAL PROTEINS FROM BACILLUS THURINGIENSIS
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                                                                                                                                                                                                                                                      Sequence 6, Application US/08622740
Patent No. 5990390
GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Kirihara, Julie A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5523211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 493,453
FILING DATE: 14-MAR-1990
;SEQ ID NO:2:
LENGTH: 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/277
FILING DATE: 19-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 102,491
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: 836,967
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: 493,453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants and Cells Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
                                                                                                                           STREET: 3500 IDS CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                   275 ITIYTDA 281
                                                                                             COUNTRY: U
                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VTFYTDA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VTFYTDA 7
                                                                                                                         M
                                                                                                                                                  E: Schwegman, L
3500 IDS Center
                                                                                                       USA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                  and Cells Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.78;
71.48;
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                                                                                                                                                          Lundberg, Woessner & Kluth,
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Pred. No. 3.
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Pred. No. 3.6e+02;
1; Mismatches 1;
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3.7e+02;
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-440-689-6
                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 55402
ZIP: 55402
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,689
FILING DATE: 15-MAY-1995
FILING DATE: 15-MAY-1995
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US-08-440-689-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application Patent No. 6025545
GENERAL INFORMATION:
                                                                                                              CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WOESSNEY, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPAN: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                       TELEFAX: 612-339-3061
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Walters, Daw APPLICANT: Kirihara, Ju TITLE OF INVENTION: Meti TITLE OF INVENTION: Proposition of INVENTION: and NUMBER OF SEQUENCES: 22 CORRESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 ITIYTDA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Minneapolis
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VENTION: Methods and Compositions for the VENTION: Production of Stably Transformed, VENTION: and Cells Thereof EQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Walters, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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             protein
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71.4%;
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71.48;

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RESULT 12
US-08-440-689-8
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Best Local S
Matches 5
                                                                                                                                                                  Sequence 8, Application US/08440689 Patent No. 6025545
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8,
                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 8:
                                               APPLICANT: Lundquist
APPLICANT: Walters,
APPLICANT: Kithara,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 27-MARCH-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.013US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339.0331
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Woessner, Warren REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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3Y: linear
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Lundquist, Ronard ...
Lundquist, Ronard ...
Walters, David A.
Walters, David A.
Kirlhara, Julie A.
Kirlhara, Julie A.
Kirlhara, Methods and Compositions for the
(INVENTION: Production of Stably Transformed, Fertile Monocot Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614 amino acids
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3500 IDS Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methods and Compositions for the Production of Stably Transformed, Fertile Monocot Plants and Cells Thereof
                                                                                                                                                                                                                                                                                                                                                         66.78;
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1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 2;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                         Mismatches
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Query Match .
Best Local Similarity
Similarity 5; Conservi
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                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 612-339-3061 INFORMATION FOR SEQ ID NO:
                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWMARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WOOSSNEY, WATTON D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                             APPLICATION NUMBER: US/09/042,426 FILING DATE: March 13, 1998 CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                CITY: Summit
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DNA Construct Containing Bacillus
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Pred. No. 3.
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                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8e+02;
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SEQUENCE CHARACTERISTICS:

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# MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis .

IMMEDIATE SOURCE:

CLONE: Bt protein

US-09-042-426-10
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                                                                                                                                        US-08-729-601A-2
                                                                                                                                                          TELEFAX: 312-3/2 NO: 2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
TYPE: amino acid
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US-08-729-601A-2
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Best Local Similarity
"atches 5; Conserv:
                                                             Matches
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08729601A Patent No. 6166302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Merlo, Donald J.
APPLICANT: Folkerts, Otto
                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 312-372-7842
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Modified Bacillus Thuringiensis Gene for TITLE OF INVENTION: Lepidopteran Control in Plants NUMBER OF SEQUENCES: 84
303 ITIYTDA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 ITIYTDA 309
                                                                                                                                                                                                                                                                                           NAME: Krueger, James P. REGISTRATION NUMBER: 35,234
REFERENCE/DOCKET NUMBER: 60
                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/729,601A FILING DATE: CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
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                              1 VTFYTDA 7
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135 S. LaSalle St.
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                                                             Conservative
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71.4%;
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                                           Score 30; DB 4; Lenglu v...
Pred. No. 3.8e+02;
""smatches 1; Indels
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Pred. No. 3.8e+02;
1; Mismatches 1
                                                                                   Length 617;
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Search completed: June 13, 2001, 14:27:07 Job time: 628 sec
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Best Local Similarity
Whiches 5; Conserve
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US-07-671-817A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/07671817A Patent No. 5424409
                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19910401
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8823068.5
FILING DATE: 30-SEP-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/671,817A
FILING DATE: 19910401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20036-3601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ely, Susan
APPLICANT: Tippett, Janet M
TITLE OF INVENTION: DNA constructs
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                      303 ITIYTDA 309
                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/
FILING DATE: 29-SEP-1989
                                                                                                          1 VTFYTDA 7
                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Cushman, Darby and Cushman STREET: Eleventh floor, 1615 L Street, N.W.
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Pred. No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                    7654
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seq length:
  protein search, using sw model
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/SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*

/SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:*

/SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*

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/SIDS6/gcgdata/geneseq/geneseqp/AA1989.DAT:*

/SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:*

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Match
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93
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Gapop 10.0 , Gapext 0.5
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Y79133
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R54816
R52807
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           Human foetal intes
Human foetal intes
Anti-hILl2 antibod
Human immunoglobul
Amino acid sequenc
N-terminal sequenc
SpA-reactive VH re
Humanised murine B
Anti-B7.1 monospec
Anti-B7.1 monospec
                                                                                                                                                                                                                                                              Description
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W94489
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| 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 63 |
|-------------|--------------------|---------|--------------------|-------|---------|--------|--------------------|--------|--------------------|---------|---------|--------------------|--------------------|--------|---------|---------|-------------|---------------|---------------|------------|--------|--------|--------------|-------------|-----------|------------|---------|---------|--------------------|-------|---------|---------|--------------------|
| 6. | ς. | | | 66.7 | 6. | | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | ς. | 66.7 | 66.7 | ა | | ٥. | ٥. | <u>ه</u> | σ. | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 67.7 |
| 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 97 | 96 | 85 | 84 | 30 | 25 | 25 | 20 | 20 | 20 | 580 |
| 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 19 | 16 | 15 | 14 | 21 | 21 | 21 | 21 | 17 | 15 | 15 | 21 | 20 | 19 | 20 |
| 666 | 4014 | 013 | B40138 | 013 | 013 | B40134 | B40130 | B40113 | B40108 | B40107 | B40096 | B40095 | B40094 | B40087 | B40086 | B40085 | B40084 | B40072 | W59614 | R72074 | R52066 | R34279 | B40112 | Y64844 | Y64735 | 4 | 704 | 279 | R52775 | 913 | 448 | W68169 | W90217 |
| tial peptid | Anti-hIL12 antibod | i-hIL12 | Anti-hIL12 antibod | 2 ant | i-hIL12 | N | Anti-hIL12 antibod | N | Anti-hIL12 antibod | i-hIL12 | i-hrr12 | Anti-hIL12 antibod | Anti-hIL12 antibod | N | i-hIL12 | i-hIL12 | i-hIL12 ant | i-hIL12 antib | -RSV F protei | VH region. | μ- | NE P | hIL12 antibo | 5' EST rela | 5' EST re | 5' EST rel | group I | e BrE-3 | Murine BrE-3 immun | adult | lt hear | G heavy | Bispecific tetrava |

ALIGNMENTS

Human foetal intestine zonulin N-terminal peptide.

W94489;

21-APR-1999 (first entry)

W94489 standard; peptide; 20

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Key Location/Qualifiers Misc-difference 16
      WPI; 1999-070123/06
                                                                      28-APR-1998;
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                    Zonulin; mammalian tight junction; zonula occludens toxin; ZOT: Vibrio cholerae; vaccine; cholera toxin; polyclonal antibody; intestinal mucosa; nasal mucosa; blood brain barrier.
                                      (UYMA-) UNIV MARYLAND BALTIMORE
                                                      21-MAY-1997;
                                                                                      26-NOV-1998
                                                                                                     W09852415-A1
                                                       97US-0859931
                                                                      98WO-US07636
                                                                                                                    /note= "unspecified"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes pure zonulin which has an apparent molecular weight of 47 kD, as determined by SDS-PAGE, which is recognised by both anti-tau polyclonal antibody and by anti-zonula occludens toxin (ZOT) polyclonal antibody, and is capable of reversibly opening mammalian tight junctions. Zonulin proteins function as physiological modulators of mammalian tight junctions. They can be used for enhancing the absorption of therapeutic agents across tight junctions of intestinal and nasal mucosa and across tight junctions of the blood brain barrier. Zonulin can be used with agents such as drugs, norepinephrine, adenosine, dobutamine, dopamine, epinephrine, nalbuphine, huntrance, phentolamine, doxapram, alfentanil, dezocin, nalbuphine, huntrance, phentolamine, doxapram, alfentanil, dezocin, nalbuphine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             buprenorphine, naloxone, ketorolac, midazolam, propofol, metacurine, midazolam, propofol, metacurine, midazolam, propofol, metacurine, wincristine, vinblastine, cytarabine, mitomycin doxorubicin, vincristine, vinblastine, methicillin, mezlocillin, piperacillin, cetoxitin, cefenicid, cefmetazole and azireonam, a hormone e.g. testoxiterone, nandrolene, menotropins, insulin, urofolitropin, interferon-lapha, interferon-beta, interferon-gamma, interfeukin-1 (II-1), II-2, II-4, II-8, polyvalent IgG, specific IgG, IgA, or IgM. The proteins can also be used for the production of antibodies which can be used to assay for zonulin in body tissue or fluids, or in affinity-purification of zonulin. The present sequence represents an N-terminal peptide of zonulin.
              Fasano A;
                                                                                   03-AUG-1998;
                                                                                                                     28-JUL-1999;
                                                                                                                                                      17-FEB-2000
                                                                                                                                                                                          WO200007609-A1
                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                  gastrointestinal inflammation; therapy
                                                                                                                                                                                                                                                                                                                                               Zonulin; antagonist; zonula occludens toxin receptor;
human; blood-brain barrier; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                     Human foetal intestine zonulin N-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2000
                                                (UYMA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Peptide; 20
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18; Conserv
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                                                MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                   98US-0127815
                                                                                                                     99WO-US16683
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                         /note= "unidentified residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%;
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Pred. No. 4.2e-06;
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                                                                                                                       Salrezu ... Kaymakcalan Z. Labkuvu.
Kaymakcalan Z. Labkuvu.
Veldman GM, Venturini
Veldman GM, Carmen
                                                                                                                                                                                             (BADI )
(GEMY )
                                                                                                      WPI; 2000-638250/61.
                                                                                                                                                                    Salfeld JG,
                                                                                                                                                                                                                                     25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                             antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the N-terminal region of foetal human intestinal zonulin. The N-terminal sequences of human adult and foetal zonulins (see Y79130-36) were compared with Vibrio.cholerae zonula occludens toxin (ZOT) to identify a common motif thought to be involved in receptor binding. Peptide antagonists (see Y79105-29) based on this motif are useful as antiinflammatory agents for treatment of gastrointestinal inflammation, and for treatment of conditions associated with breakdown of the blood-brain
                                                                                                                                                                                                                                                             24-MAR-2000; 2000WO-US07946.
                                                                                                                                                                                                                                                                                                                 WO200056772-A1
                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; neutralising antibody; interleukin-12; IL-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-hII12 antibody H chain V region amino acid sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B40074;
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B40074 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigeliosis, viral gastroenteritis, meningitis, encephalomyelitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           barrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLQLAESGGVLVQPGXSDRL
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                                                                                                                                                                                            BASE AG.
GENETICS INST INC.
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                                                                                                                                                     Roguska M, Pasl
Z, Labkovsky B,
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                                                                                                                             S, A
                                                                                                                                                                 Paskind M,
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                                                                                                                            Warne
Smith
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                                                                                                                                                                                                                                                                                                                                                                                                         region;
                                                                                                                           kind M, Banerjee S, Tracey DE
"Sakorafas P, Friedrich S, M
arne NW, Widom A, Elvin JG,
mith S, Holtet TL, Du Fou SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                      leukin-12; IL-12; antiinflammatory; CDR; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitis, encephalomyelitis
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4.2e-06;
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                                                                                                                                                               White M;
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This invention

a new

human

antibody specific

for

humar

Page

121; relates to

377pp;

English.

New human antibody specific for treat disorders characterized of disease and multiple sclerosis

for human interleukin-12 (IL-12) used to ad by aberrant IL-12 expression e.g. Crohn's is -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc interleukin-12 (IL-12). The invention also includes antigen binding cportions that bind to IL-12. Sequences B39485-B39516 represent human cc anti-IL-12 antibody heavy and light chain complementarity determining cc anti-IL-12 antibody heavy and light chain complementarity determining cc region (CDR) amino acid sequences, and also includes variable region amino acid sequences are given in B39517-B39560 and B40068-B40149. Sequences B39772-B40063 crepresent anti-IL-12 CDR3 related amino acid sequences, B39772-B40063 crepresent other CDR sequences. Light chain CDR3 consensus sequences are given in B40064-B40067. Primers used in the identification and CC construction of the antibodies of the invention are given in CC construction of the antibody of the invention is a neutralising antibody cand has antirheumatic; antiarthritic; antisclerotic; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antibacterial and immunosuppressive activity. Sepecially Crohn's classes, multiple selevosts and repumatorial architis. They can also be called to the manifest traces and architists.
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Best Local S
Matches 14
Protein sequences (R66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (078939-79002) were isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers 078917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer; cosmid;
                                                                                                                                                                                     Claim 50; Page 85-87; 130pp; Japanese.
                                                                                                                                                                                                                                          DNA fragment comprising human immunoglobulin vh production of human immunoglobulin in mammalian
                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                         Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in the manufacture of a pharmaceutical composition to treat human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL-12 disorders.
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                                                                                                                                                                                                                                                                                                                          1995-006791/01.
DB; Q78981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; amplify; human; immunoglobulin; variable; heavy chain; placenta; vector; pJB81; E.coli; mammalian.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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73.7%;
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Pred. No.
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0.0036;
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RESULT
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Best Local S
Matches 14
                            This is the amino acid sequence of the human D7.2 heavy chain variable region, used in the method of the invention. for providing receptors that can be used for targeting antigens in humans without being immunogenic themselves. Such receptors can be used for treating diseases such as tumours or auto-immune diseases, graft rejection after transplantation, infectious diseases by targeting cellular receptors as well as allergic, inflammatory, endocrine and receptors as well as allergic, inflammatory, endocrine and
                                                                                                                                                                                          Production of anti-human antigen receptors -combination of functionally rearranged VH and chains expressed from a recombinant vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJB81. The ligation products were in vitro packed and infected into E.coli 490A. The fragments were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
Sequence
                                                                                                                                                                 Claim 9;
                                                                                                                                                                                                                                               WPI; 1998-594564/50
N-PSDB; V68538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W80816
                                                                                                                                                                                                                                                                                         Kufer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9846645-A2
                           pathological
                                                                                                                                                                                                                                                                                                                     (RAUM/) RAUM T.
                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour; auto-immune disease; graft rejection; allergy;
inflammatory disease; endocrine disease; degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of human D7.2 heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                               14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; D7.2 heavy chain variable region; receptor; antigen;
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                                                                                                                                                               Fig 8; 84pp; English.
                                                                                                                                                                                                                                                                                           Raum
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124
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                           process.
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73.7%;
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                                                                                                                                                                                                      serecting a immunoglobulin
                                                                                                                                                                                                                     selecting
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Best Local Similarity

73.78;

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RESULT
Y84660
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            The present sequence represents the N-terminal of a human zonulin college to polypeptide. The specification describes a method of suppressing antigen presenting cell (APC)-mediated lymphocyte proliferation in a mammalian host pre-exposed to a particular antigen. The method comprises administering to the host an effective amount of a zot-related from the control of the APC. The method can be used to down-regulate the activity of the APC. The method can be used to down-regulate APC-mediated lymphocyte proliferation in mammalian hosts suffering from auto-immune or immune-related collisorders, immune system rejection subsequent to tissue or organ collisorders, immune system rejection subsequent to tissue or organ collisorders, insulin dependent diabetes mellitus, celiac disease, 3) or inflammatory or allergic diseases. The auto-immune collisorders include multiple sclerosis, rheumatoid cor immune related disorders include multiple sclerosis, rheumatoid corrected and the related disorders include multiple sclerosis, rheumatoid corrected disorders include multiple sclerosis rheumatoid corrected disorders include multiple sclerosis rheumatoid corrected disorders include multiple sclerosis rheumatoid disorders include multiple sclerosis rheumatoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suppression of antigen presenting cell mediated lymphocyte proliferation, by administering a Zot-related immunoregulator useful for treating immune-related disorders, immune system rejection
     thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; insulin dependent diabetes mellitus; celiac disease; Sjogren's syndrome; systemic lupus erythematosus; auto-immune thyroiditis; idopathic thrombocytopenic purpura; hemolytic anemia; Grave's disease; Addison disease; autoimmune orchitis; hemolytic anemia; vasculitis; autoimmune coagulopathy; polymyositis; myasthenia gravis; polymeuritis; pemphigus; rheumatic carditis; permatomyositis; scleroderma; asthma; psoriasis; eczematous dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APC; lymphocyte proliferation; antigen; auto-immune disorder; immune-related disorder; immune system rejection; multiple sclerosis; organ transplantation; inflammatory disease; allergic disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sarcoma; inflammatory bowel disease; proliferative disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                             95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                             or organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "any amino acid"
  thrombocytopenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanner MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein of 47
purpura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     system rejection
hemolytic anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT
R54816
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Best Local
                       A B-cell superantigen (sAg) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The sAg is used to enhance production of VH, especially VH3, restricted Abs. During attempts to identify sAgs, aa sequences (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and DNA sequences (R54802-16, Q64842-56) of VH regions of SpA binders obtained from combinatorial libraries were determined.
                                                                                                                                                                   Stimulating prodp. of variable region gene family restricted antibodies - through B-cell super-antigen vaccination
Sequence
                                                                                                                                        Disclosure; Page 113; 130pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  superantigen;
VH; protein-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyneuritis, pemphigus, rheumatic carditis, polymyositis, Dermatomyositis, and scleroderma. The inflammatory or allergic disease or disorder is selected from asthma, psoriasis, eczematous dermatitis,
                                                                                                                                                                                                             N-PSDB; Q64856.
                                                                                                                                                                                                                                                                                                              30-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SpA domain D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SpA-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R54816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R54816 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or disorder is selected from asthma, psorlasis, eczematous dermati
Karposi's sarcoma, multiple sclerosis, inflammatory bowel disease,
proliferative disorders of smooth muscle cells, and inflammatory
                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                     11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                               WO9409818-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grave's disease, Addison disease, autoimmune orchitis, pernicious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LQLAESGGVLVQPGXSDRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-A;
                                                                                                                                                                                                                           1994-167127/20
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98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig binding region; B-cell superantigen; sAg;
heavy chain variable region; VH3 restricted antibody;
, VH26C; combinatorial library; B-lymphocyte;
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73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with mycotic, viral, parasitic, or bacterial
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                                                                                                                                        English.
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Best Local Similarity Matches 15; Conserv

Conservative

68 78

. 98;

Score 64; DB Pred. No. 0.00 0; Mismatches

DB .0073;

Length 98;

Indels

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Gaps

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Query Match

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RESULT
R52807
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                                                                                                                                16-NOV-1992;
30-SEP-1993;
08-OCT-1993;
                                                                         WPI; 1994-183510/22.
N-PSDB; Q62791.
                          Claim 4;
                                         New analogue peptide(s) comprising antibody variable regions used to develop prods. for use in the detection, diagnosis, therapy and prevention of neoplasms
                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
                                                                                                                 (CANC-) CANCER
                                                                                                                                                                16-NOV-1993;
                                                                                                                                                                                26-MAY-1994
                                                                                                                                                                                               WO9411509-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric antibody; human mammary fat globule; human breast carcinoma; murine anti-HMFG monoclonal antibody BrE3; humanised analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised murine BrE3 immunoglobulin heavy chain V-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R52807;
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                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin variable domain; primer; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
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different regions of the mature polypeptide R52807 Features Table are preferred partial sequences for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQLAESGGVLVQPGXSDRL 20
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| 1qllesggglvqpggslrl 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                 RĽ,
                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
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                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                92US-0977696.
93US-0129930.
93US-0134346.
                                                                                                                 RES FUND CONTRA COSTA.
                                                                                                                                                                93WO-US11445
                                                                                                 Couto
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20..49
                                                                                                                                                                                                                       /label-
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                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                       /note= "Claim 4"
                                                                                                                                                                                                                                                                     /label- FR3
                                                                                                                                                                                                                                                                                              /label- CDR2
                                                                                                                                                                                                                                                                                                            /note- "Claim
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                         109pp;
                                                                                                                                                                                                                                                                                                                                                                   abel- FR1
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                         English
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                                                                                                 Padlan EA,
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                                                                                                 Peterson
          indicated
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antineoplastic

This polypeptide comprises a B7-24 monospecific triabody composed of the VH region of anti-B7.1 monoclonal antibody (MAb) B7-24 joined to the VL region of B7-24. A triabody is a mono- a bi- or

Example 7.3; Fig

32; 182pp; English.

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RESULT
W90225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analogue peptides. The peptides selectively bind to an antigen on the surface or in the cytoplasm of a neoplastic cell. They comprise at least one CDR and at least one V region of L- or H-chains from an anti-human mammary fat globule antigen antibody (i.e. murine BrE3 antibody) but where I to 46 amino acids in the FRs are substituted by their homologues from human antibodies (humanised). The humanised antibody is useful for carcinoma therapy and diagnosis and for in vivo imaging of neoplastic cells. It is also of use in inhibiting the
                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                          B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease;
                                                                                                                                 Bosman A,
                                                                                                                                                                                                                                                                                                                                                                                                                  allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W90225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W90225 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                             New molecules which bind B7.1 and B7.2 - useful to immune diseases including allograft rejection
                                                                                                           WPI; 1999-105615/09
                                                                                                                                                       (INNO-) INNOGENETICS
                                                                                                                                                                              20-JUN-1997;
                                                                                                                                                                                                   22-JUN-1998;
                                                                                                                                                                                                                        30-DEC-1998
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                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                 Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-B7.1 monospecific triabody B7-24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth of a primary or metastasised neoplasm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LQLAESGGVLVQPGXSDRL
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21 vqlvesggglvqpggsmrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                  X01659.
                                                                                                                                                                                                                                                                                                                                                                                                               therapy; human;
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248..25
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139..247
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                                                                                                                                                                                                                                                                                                                                     /note= "pelB signal peptide"
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73.78;
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                                                                                                                                  Lorre
                                                                                                                                                                                                                                                                                         "anti B7.1 MAb
                                                                                                                                                                                                                                                                    "His6 tag"
                                                                                                                                                                                                                                                                                                                                                                                                                triabody; antibody; B7-24.
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Pred. No. 0.015;
                                                                                                                                  Sablon
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                                                                                                                                 E
                                                                                                                                                                                                                                                                                         VL region"
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RESULT

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Query Match
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and one B7.1 molecules. It has a rigid structure that prevents simultaneous binding to the 3 targets. Each antigen-binding site is formed by pairing of one VH and one VL domain from the same or from two different polypeptides. The invention relates to novel molecules, including triabodies, which can cross-link and/or cross-react with the costimulatory molecules B7.1 and B7.2 expressed on professional antigen-presenting cells, leading to the inhibition of antigen-specific T cell activation. Methods are provided for the production of such B7-binding molecules, and for their use in the treatment or prevention of diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; diabody; antibody; B7-24.
    New molecules which bind B7.1 and B7.2 • useful to prevent and treat immune.diseases including allograft rejection
                                                                                                                      Bosman A,
                                                                                                                                                               (INNO-) INNOGENETICS
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                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                      Buyse M,
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139..14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "pelB signal peptide"
25..138
                                                                                                                                                                                                                                                                                                                                                                                   253..258
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "anti B7.1 MAb VL region"
                                                                                                                                                                                                                                                                                                                                                                                                                         144..252
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                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-
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73.7%;
                                                                                                                        Lorre
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "G4S flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "anti B7.1 MAb VH region"
                                                                                                                                                                                                                                                                                                                                                             "His6 tag"
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Pred. No. 0.
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                                                                                                                        Sablon
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0.029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
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ID W9021B
XX W9021B
AC W9021B
XX 10-MAY
XX B7 bin
KW CD86;
KW CD86;
KW CD86;
KW Lransp
KW B1habl
XX Chimer
OS Chimer
OS Chimer
XX Chimer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide comprises a B7-24 monospecific diabody composed of the VH region of anti-B7.1 monoclonal antibody (MAb) B7-24. To joined via a short, flexible linker to the VL region of B7-24. Charles or bispecific bivalent molecules are generated by shortening the flexible linker sequence between the VH and VL of the anti-B7.1 color bispecific molecules by cross-pairing the VH and VL of the anti-B7.1 color bispecific molecules by cross-pairing the VH and VL domains of the product of the anti-B7.2 color bispecific molecules by cross-pairing the VH and VL domains of the 2 scFvs with different antigen recognition (B7.1/B7.2 and CR br.12/B7.12). The invention relates to novel molecules, including CR br.12/B7.12. The invention relates to novel molecules, including CR diabodies, which can cross-link and/or cross-react with the costimulatory molecules B7.1 and B7.2 expressed on professional antigen-presenting cells, leading to the inhibition of antigen-production of such B7-binding molecules, and for their use in the creatment or prevention of diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                Region
                                                                                                                                                                                                                                                                                                                                                                                                Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergy; therapy;
BiTAb1G10-B7-24H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; bispecific tetravalent antibody; BiTAb;
                                                                                                                                       Domain
                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W90218;
                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bispecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W90218 standard; Protein; 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7..2; Fig 24; 182pp; English.
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24 vqlqesggglvqpggsrrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LQLAESGGVLVQPGXSDRL
                                                                                                                                                                                                                                                                                                                                                                                              synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tetravalent antibody BiTAb1G10-B7-24H6
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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no sapiens.
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                                                                                             /note= "1
306..426
                                                                                                                                                                                                                                    136..248
/note= "VL
                  442..550
                                                        427..441
                                                                                                                                       286..305
                                                                                                                                                                              260..285
                                                                                                                                                                                                                   249..259
                                                                                                                                                                                                                                                                                              /note= "VH region anti B7.2 MAb"
121..135
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                            /note=
                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                              /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.78;
73.78;
                                   "(G4S3)flexible linker"
                                                                                                              "human IgG3 hinge domain"
"VL region anti B7.1 MAb
                                                                        "VH region
                                                                                                                                                                                             "human IgG3 hinge region"
                                                                                                                                                                                                                                                                           "(G4S3) flexible linker"
                                                                                                                                                       "helix-turn-helix dimerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                    region anti B7.2 MAb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                          anti B7.1 MAb'
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Gaps

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Length 258; Indels

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RESULT 12
W90217
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises the bispecific tetravalent antibody

BiTAb1G1D-B7-24H6. The molecule consists of 4 scFvs, i.e. 2

anti B7.1 scFvs and 2 anti B7.2 scFvs (tetravalency). One single

BITAb is a homodimer of 2 identical molecules, each containing both

c and anti B7.1 scFv are linked using a dimerisation domain (see

M90219), which drives the homodimerisation of the molecule. DNA

(see x01552) encoding the BiTAb has been constructed to allow

expression of the BiTAb in transformed E. coli cells. The BiTAb

cross-links, and/or cross reacts, with the costinulatory molecules

B7.1 and B7.2 that are expressed on the membrane of professional

antigen-presenting cells, leading to the inhibition of antigen-

specific T cell activation. The invention relates to such

B7-binding molecules, methods for their production, and their use

for treating or preventing diseases of the immune system, in

particular graft rejection, graft versus host disease, allergy and
                          Chimeric - Mus sp.
Chimeric - Homo sa
                                                                                 B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; allograft rejection; allograft specific tetravalent antibody; B1TA allorgy; therapy; human; bispecific tetravalent antibody; B1TA
                                                                     allergy; therapy; human; BiTAbB7-24-1G10H6.
                                                                                                                                                           Bispecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1998
                                                                                                                                                                                        10-MAY-1999
                                                                                                                                                                                                                      W90217
                                                                                                                                                                                                                                                 W90217 standard; Protein; 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7.1; Fig 18; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-105615/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                          312
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:|| |||| ||||| | ||
                                                                                                                                                                                                                                                                                                                        vqlqesggglvqpggsrrl 330
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                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 73.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buyse M,
                                                                                                                                                         tetravalent antibody BiTAbB7-24-IG10H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         556 AA;
                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                               67.78;
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1; Mismatches
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0.068;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 556
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W90219), which drives the homodimerisation of the molecule. DNA (see X01651) encoding the BITAb has been constructed to allow expression of the BITAb in transformed E. coli cells. The BITAb cross-links, and/or cross-reacts, with the costimulatory molecules 97.1 and B7.2 that are expressed on the membrane of professional antigen-presenting cells, leading to the inhibition of antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods for their production, and their use for treating or preventing diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).
                                                                                                                                                                                                                                                  This polypeptide comprises the bispecific tetravalent antibody BiTAbB7-24-IG10H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2 anti B7.2 scFvs (tetravalency). One single BiTAb is a homodimer of 2 identical molecules, each containing both an anti B7.1 and anti B7.2 scFv (bispecificity). An anti-B7.1 and and anti-B7.2 scFv are linked using a dimerisation domain (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7.1; Fig 16; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INNO-) INNOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1997;
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261
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154..262
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263..27
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25..138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "human IgG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "human IgG3 hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "(G4S3) flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "VH region anti B7.1 MAb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "codons for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "VH region anti B7.2 MAb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "helix-turn-helix dimerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "codons for these amino acids are not
present in the DNA sequence for
BTiTAbB7-24-1G1-H6 provided in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification"
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Query Match

73.78;

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RESULT 13
W68169
                                                                                                                                                                CC (19G) heavy chain, IG V-III region (HV3T), An IgG derived peptide sequence from the human immunoglobulin GC (19G) heavy chain, IG V-III region (HV3T), An IgG derived peptide CC sequence having similarity to this sequence has a stimulating effect on CC the fibrinolytic activity of the scuPA/suPAR complex of the invention. The invention provides a thrombolytic therapeutic composition for the CC treatment and prevention of a thrombolytic disorder associated with CC the formation of fibrin clots. The composition comprises, as the active ingredient, a complex of a single chain urokinase type plasminogen activator (scuPA) and a soluble urokinase plasminogen activator receptor CC (suPAR). The complex (scuPA/suPAR) has thrombolytic activity under physiological conditions and in the presence of IgG, or of at least 1 IgG-derived peptide, and induces fibrinolysis of fibrin clots. The CC compositions and complex are useful for the treatment or prevention of CC compositions and complex are useful for the formation of fibrin clots, especially myocardial infractions, cerebro-vascular events, pulmonary cc embolism and deep vein thrombosis.
                                                                      Query Match
Best Local
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 73.7 Matches 14; Conservative.
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compositions with thrombolytic activity for, e.g. treatment of thromboembolism - comprise complex of single chain urokinase type plasminogen activator, scupA, and soluble urokinase plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombolytic activity; soluble urokinase plasminogen activator receptor; single chain urokinase type plasminogen activator; thromboembolism; scupA; supAR; IgG; regulator; fibrinolytic activity; fibrin clot; myocardial infraction; cerebro-vascular event; pulmonary embolism; deep vein thrombosis; immunoglobulin; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 25; 46pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-348262/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                  Local Similarity
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                                                                                                                                       20
                                                   Conservative
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                                                                  66.78;
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                                                                  Score 62; DB 19; Length 20; Pred. No. 0.0027;
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1; Mismatches
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Query Match
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                                                                                                                                                                                                                                                                               interferon-alpha, interferon-beta, interferon-gamma, interleukin-1 (IL-1), IL-2, IL-4, IL-8, polyvalent IgG, specific IgG, IgA, or IgM. The proteins can also be used for the production of antibodies which can be used to assay for zonulin in body tissue or fluids, or in affinity-purification of zonulin. The present sequence represents an N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      buprenorphine, naloxone, ketorolac, midazolam, propofol, metacurine, mivacurium, succinylcholine, cytarabine, mitomycin doxorubicin, vincristine, vinblastine, methicillin, mezlocillin, piperacillin, cetoxitin, cefenicid, cefmetazole and aztreonam, a hormone e.g. testosterone, nandrolene, menotropins, insulin, urofolitropin, testosterone, nandrolene, menotropins, insulin, urofolitropin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified zonulin - which is capable of reversibly opening mammalian tight junctions, used for enhancing the delivery of across intestinal and nasal mucosa and blood brain barrier
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 45; 64pp;
                                                                                                                                                                                                                                                            peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1999
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                                            Similarity
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       Conservative
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                                     66.7%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
   1;
                                        Score 62;
Pred. No.
       Mismatches
                                            0
                                                                          DB 20;
                                        0027;
                                                                  Length 20;
   Indels
   0;
Gaps
   0;
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Search completed: June 13, 2001, 14:25:46 Job time: 665 sec
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                                                                                                                                                                                                                RESULT 15
Y79130
                                                                                                                                      Query Match 66.7%;
Best Local Similarity 73.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                        The present sequence is that of the N-terminal region of adult human heart zonulin. The N-terminal sequences of human adult and foetal zonulins (see Y79130-36) were compared with Vibrio cholerae zonula occludens toxin (ZOT) tidentify a common motif thought to be involved in receptor binding. Peptide antagonists (see Y79105-29) based on this motif are useful as antiinflammatory agents for treatment of gastrointestinal inflammation, and for
                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigeliosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zonulin; antagonist; zonula occludens toxin receptor; human; blood-brain barrier; antiinflammatory; gastrointestinal inflammation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y79130 standard; Peptide; 20 AA.
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                            treatment of conditions associated with breakdown of the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 6; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-205565/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fasano A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adult heart zonulin N-terminal sequence.
                                                                        2 LQLAESGGVLVQPGXSDRL 20
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2 vqlvesggglvqpggslrl 20
                                                                                                                                                                                                                20 AA;
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                                                                                                                                      Score 62; DB 21; Length 20; Pred. No. 0.0027; 1; Mismatches 4; Indels
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| 62 | 62 | 62 | 62 | 62 | 6 2 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 | 62 |
| 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 |
| 125 | 124 | 123 | 123 | 123 | 121 | 121 | 121 | 120 | 120 | 119 | 119 | 118 | .117 | 117 | 117 |
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| S30531 | S20775 | S30532 | S26794 | S31509 | S31104 | S31118 | S26798 | G1HUDB | M3HUBW | S31107 | G1HUTE | S31121 | S21980 | S36259 | A34964 |
| Ig heavy chain V r | Ig heavy chain V r | Ig heavy chain V r | Ig heavy chain V r | chain | 7 | | | | • | chain | Ig heavy chain V-I | • | Ig heavy chain V-g | | Ig heavy chain pre |
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Ig heavy chain V region (DP-33) - human (fragment)
C:Species: HOmo sapiens (man)
C:Species: HOmo sapiens (man)
C:C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26929
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty growth for the properties of human sermine V(H) sequences reveals about fifty growth for the preliminary A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12335; NID:g32889; PIDN:CAA78205.1; PID:g32890
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heteroctetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33·14q32.33
C;Superfamily: immunoglobulin V region; immuno C;Keywords: heterotetramer; immunoglobulin F:15-98/Domain: immunoglobulin homology <IMM>F;22-96/Disulfide bonds: #status predicted
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Alfuzp

Ig heavy chain V-III region (Zap) - human (tentative sequence)

C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C;Accession: A02061

R;Capra, J.D.; Kehoe, J.M.

R;Capra, J.D.; Kehoe, J.M.

Proc. Natl. Acad. Sci. U.S.A. 71, 845-848, 1974

Proc. Natl. Acad. Sci. U.S.A. 71, 845-848, 1974

A;Title: Variable region sequences of five human immunoglobulin heavy chains
A;Reference number: A93794; MUID:74142702

A;Accession: A02061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-116 <CAP>
C:Comment: This chain was isolated
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LQLAESGGVLVQPGXSDRL 20
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Pred. No. 0.00036;
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: $44111
R;HawKins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma :rescue of var A;Reference number: $44105
A;Reference number: $44105
A;Residues: DNA
A;Residues: 1-120 CHAW>
A;Residues: EMBL:Z31387; NID:q472965; PIDN:CAAB3262.1; PID:g940522
RESULT 5
PH0116
Ig heavy chain precursor V-D-J region (JP-FL-2) -C:Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;20-147/Product: Ig heavy chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain precursor V-D-J region (JP-FL-6) - human C;Species: Homo sapiens (man) C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_c c;Accession: PH0120 R;Zelenetz, A.D.; Chen, T.T.; Levy, R. J. Exp. Med. 173, 197-207, 1991 A;Title: Histologic transformation of follicular lymphoma A;Reference number: PH0115; MUID:91086845 A;Accession: PH0120
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A; Residues: 1-147 <ZEL>
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Best Local (
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Best Local Similarity
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Best Local
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73.7%;
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73.7%;
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73.7%;
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Pred. No. 0.00079;
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Pred. No.
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Pred. No. 0.00
2; Mismatches
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                                                                                                                                                                                                            Length 147;
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                                            A; Molecule type:
A; Residues: 1-148
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Best Local S
Matches 14
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Ig heavy chain precursor V-D-J region (JP-FL-4) - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-1996
C;Accession: PH0118
R;Zelenetz, A.D.; Chen, T.T.; Levy, R.
J. Exp. Med. 173, 197-207, 1991
A;Title: Histologic transformation of follicular lymphoma to diffuse lymphoma realizable in transformation of follicular lymphoma to diffuse lymphoma realizable in translation not shown
A;Reference number: PH0115; MUID:91086845
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-148 <ZEL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;10-148/Froduct: Ig heavy chain #status predicted <MAT'>
F;34-117/Domain: immunoglobulin homology <IMM>
   C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                  R:Zelenetz, A.D.; Chen, T.T.; Levy, R.
J. Exp. Med. 173, 197-207, 1991
A:Title: Histologic transformation of follicular lymphoma
A;Reference number: PH0115; MUID:91086845
A;Accession: PH0115
                                                                                                                                 A; Status: translation not shown
                                                                                                                                                                                                                                                                                                               Ig heavy chain precursor V-D-J region (JP-FL-1) - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #tex:
C;Accession: PH0115
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A; Residues: 1-148 <ZEL>
A; Residues: 1-148 <ZEL>
C; Superfamily: immunoglobulin V region; immunoglobulin h
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-148/Product: Ig heavy chain #status predicted <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
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C;Accession: PH0116
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Best Local Similarity
Matches 14; Conserv
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73.7%;
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73.7%;
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; Pred. No. 0.00
1; Mismatches
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Pred. No. 0.0021;
1; Mismatches
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0.0021;
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predicted <SIG>

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Ig heavy chain precursor V-D-J region (JP-FL-7) - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-1996
C:Accession: PH0121
                                                                                                                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin h C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>E;20-148/Product: Ig heavy chain #status predicted <WAT>F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                          R:Zelenetz, A.D.; Chen, T.T.; Levy, R.
J. Exp. Med. 173, 197-207, 1991
A;Title: Histologic transformation of follicular lymphoma to A;Reference number: PH0115; MUID:91086845
A;Accession: PH0119
A;Status: translation not shown
A;Residues: 1-148 <ZEL>
A;Residues: 1-148 <ZEL>
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PH0121
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C:Date: 30-Sep-1991 #sequence_revision
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A;Molecule type: DNA
A;Residues: 1-148 <ZEL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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F;34-117/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 173,
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Best Local S
Matches 14
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Best Local Similarity
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LQLVESGGGLVQPGGSRKL 39
                                      LQLAESGGVLVQPGXSDRL 20
                                                                           Similarity 73.7
14; Conservative
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73.7%;
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Pred. No. 0.
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Pred. No.
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Pred. No.
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                                                                                                                DB 2; Length 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0021;
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                                                                           Gaps
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Ig heavy chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
C;Accession: PH0872
C;Accession: PH0872
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot A;Reference number: PH0862; MUID:92078875
A;Accession: PH0872
A;Molecule type: DNA
A;Residues: 1-97 <MAN>
A;Residues: 1-97 <MAN>
A;Residues: 1-97 <MAN>
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;30-35/Region: complementarity-determining 1
F;49-66/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-148 <ZEL>
A; Residues: 1-148 <ZEL>
C; Superfamily: immunoglobulin V region; immunoglobulin ho
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: signal sequence #status predicted <SIG>
F; 21-19/Domain: ighaavy chain #status predicted <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
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c.Date: 30-Sep-1991 #sequence_revision
c.Accession: PH0117
R.Zelenetz, A.D.; Chen, T.T.; Levy, R.
J. Exp. Med. 173, 197-207, 1991
Ig heavy chain V region (DP-48) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26890
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty A;Reference number: S26885; MUID:93021117
A;Status: preliminary
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PH0872
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Best Local S
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Best Local Similarity
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73.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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0.0021;
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                                                                             reveals about fifty groups
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A; Molecule type: DNA
A; Residues: 1-97 <TOWN:
A; Residues: 1-97 <TOWN:
A; Cross-references: EMBL: Z12348; NID: g32916; PIDN: CAA78218.1; PID: g32917
A; Cross-references: EMBL: Z12348; NID: g32916; PIDN: CAA78218.1; PID: g32917
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                               F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2
                                                                                                                                                                                                                                      A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, A;Note: the sequence shows the V region (TD-Vp) from one of five DNA rearrangement C;Superfamily: immunoglobulin V region; immunoglobulin bomology C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
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A;Accession: PL0121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V-III region (TD-Vp) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (YAC-5) - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S46462
C;Accession: S46462
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela,
Nature Genet. 7, 162-168, 1994
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S46462
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A; Residues: 1-98 <BIR>
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A; Residues: 1-97 <COO>
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Best Local S
Matches 14
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Best Local Similarity
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Best Local
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LQLAESGGVLVQPGXSDRL 20
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73.78;
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Pred. No. 0.0029;
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                                                Pred. No. 0.0
L; Mismatches
                                                                    Score 62; DB 2;
Pred. No. 0.003;
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A;Cross-references: EMBL:Z12354; NID:g32930; PIDN:CAA78224.1; PID:g32931 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, AI A;Note: the sequence shows the 'region (TD-Vr) from a nonproductive DNA rearrangeme R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. J. Mol. Biol. 227, 776-798, 1992

J. Mol. Biol. 227, 776-798, 1992

A;Tittle: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885; MUID:93021117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V-III region (TD-Vr) - human (fragment) C; Species: Homo sapiens (man) C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change C; Accession: PLO123; S26897 R; Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J. J. Exp. Med. 168, 229-245, 1988
Search completed: June 13, 2001, 14:23:12 Job time: 743 sec
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A; Residues: 1-98 < TOM>
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A; Residues: 1-98 <BIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobu
A;Reference number: PL0116; MUID:88286083
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Best Local S
Matches 14
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                                                                                                                                                                                                   2 LQLAESGGVLVQPGXSDRL 20
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                                                                                                                                                                                                                                                         Score 62; DB 2;
Pred. No. 0.003;
1; Mismatches
                                                                                                                                                                                                                                                                                                               Length 98;
                                                                                                                                                                                                                                                            Indels
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rearrangemen
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Title:
Perfect score:
Sequence:
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13.285 Million cell updates/sec
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HV3T_HUMAN
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HV30_HUMAN
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P01778;
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 3 4 |
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| 5 4 | 54 | 55 | 55 | 55 | 55 | 55 | 55 | 55 | 55 | 55 | 55 |
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| HV02_CANFA | HV36_MOUSE | HV26_MOUSE | HV01_RAT | HV3A_HUMAN | HV55_MOUSE | HV54_MOUSE | HV33_MOUSE | HV32_MOUSE | HV34_MOUSE | HV31_MOUSE | HV30_MOUSE |
| P01785 canis famil | P01806 mus musculu | | | P01762 homo sapien | | mus | 8nm | P01801 mus musculu | mus | mus | |

ALIGNMENTS

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RRR ROCC OCC DTT DTC
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P01781;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-HDAVY CHAIN V-III REGION GAL.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
McBI_TaxID=9806;
SEQUENCE.
MEDLINE-75059123; PubMed-4803843; Watanabe S., Barnikol H.U., Horn
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN.
PIR; A02061; A1HUZP.
HSSP; P01772; 2IG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION ZAP.
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73.78;
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Pred. No. 0.0001;
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    Bertram J.,
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RESULT 4
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HSSP; P01772; Z1C2.
InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
NON_TER 119 119
HV3E_HUMAN
P01766;
21-JUL-1986
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
NON_TER 116 116
SEQUENCE 116 AA; 12730
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; vercon.
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
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P01777;
                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                           MEDLINE-74142702; PubMed-4522793;
Capra J.D., Kehoe J.M.;
"Variable region sequences of five human immuno
of the VH3 subgroup: definitive identification
                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V-III REGION TEI.
                                                                                                                                                                                                                                                                  hypervariable regions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1975)
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                                                                    MISCELLANEOUS:
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llarity 73.7%;
Conservative
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01, Created)
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73.7%;
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Pred. No. 0.0011;
L; Mismatches
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Pred. No.
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                   PRT;
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                                                                                                                                                              7E24DC852C7290A9 CRC64;
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Matches 14
PIR; A02065; GHUDB.
InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
NON_TER 120 120
SEQUENCE 120 AA; 13440
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Immunoglobulin V region.
NON_TER 120 120
SEQUENCE 120 AA.
                                                                 Biochemistry 18:4054-4067(1979).

''- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN.

HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INDISULFIDE BONDS.
                                                                                                                        MEDLINE=80020920; PubMed=114208; Steiner L.A., Lopes A.D.; "The crystallizable human myelom"
                                                                                                                                                                             Steiner L.A., Garcia Pardo A., Margolies M.N.; "Amino acid sequence of the heavy-chain variable region crystallizable human myeloma protein Dob."; Biochemistry 18:4068-4080(1979).
                                                                                                                  deletion.";
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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21-JUL-1986 (Rel. 01, Last s
15-JUL-1999 (Rel. 38, Last a
IG HEAVY CHAIN V-III REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              individual patient. III. The complete amanusegion of the IgM paraprotein.";
Immunochemistry 13:995-999(1976).
-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED SERUM OF A PATIENT WITH MALIGNANT LYMPH
                                                                                                                                                              CRYSTALLIZATION
                                                                                                                                                                                                                             MEDLINE=80020921; PubMed=114209;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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13440 MW;
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ا
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73.78;
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Query Match

66.7%;

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RESULT 6
HV3D_HUMAN
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PIR; A02048; H3HUTL.
InterPro; IPR003006; -.
Pfam; PF00047; 1g; 1.
Immunoglobulin V region.
Inc. mrp 115 115
                                                                                                                                                                                                                                                                                                                                       Carassius auratus (Goldfish).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Cyprininae; Carassius.

NCBI_TaxID-7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV05_CARAU STANDARD; PRT; 116 AA. P19181; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG HEAVY CHAIN V REGION 5A PRECURSOR.
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Wang A.-C., Wang I.Y., Fudenberg H.H.;
Wang A.-C., Wang I.Y., Fudenberg H.H.;
Wang A.-C., Wang I.Y., Fudenberg H.H.;

Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.*;

J. Biol. Chem. 252:7192-7199(1977).

I-I- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL CAMMORATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
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P01765;
                                                                                                                                                                        MEDLINE-88144476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable region
and family relationships of two genes and a
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Immunoglobulin V re
                                  Proc. Natl. Acad. Sci. |
PIR; B28966; B28966. .
InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last of
15-JUL-1999 (Rel. 38, Last of
IG HEAVY CHAIN V-III REGION
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        region; Signal.
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Immunoglobulin V region.
NON_TER 116 116
SEQUENCE 116 AA; 12431 MW;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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A02062; AlHUTU.
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MEDLINE-74142702; PubMed-4522793;
Capra J.D., Kehoe J.M.;
"Variable region sequences of five human immunoglobulin heavy chains
of the VH3 subgroup: definitive identification of four heavy chain
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
BY SIMILARITY.
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0.0016;
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                                                                               InterPro: IPR003006; -. Pfam; PF00047; 19; 1. Immunoglobulin V region. NON_TER 117 AA 17
                                                                                                                                                                         Capra J.D., Kehoe J.M.;
Capra J.D., Kehoe J.M.;
"Variable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup: definitive identification of four heavy chain hypervariable regions.";
Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                    PROTEIN.
PIR; A02059; G1HUWS.
HSSP; P01772; 2IG2.
                                                                                                                                                                                                                                                                                                                                                    HV30_HUMAN STANDARD; PRT; 1901776; P01776; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence up 15-JUL-1999 (Rel. 38, Last annotation IG HEAVY CHAIN V-III REGION WAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        MEDLINE-74142702; PubMed-4522793;
Capra J.D., Kehoe J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
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Immunoglobulin V region; Signal.
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                                     Local
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2 LQLAESGGVLVQPGXSDRL 20
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117 AA; . 12582 MW;
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73.7%;
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                     Score 61; DB Pred. No. 0.00 1; Mismatches
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Pred.
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                                                                                    201DEF0E1E53D9BF CRC64;
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red. No. 0.0016;
Mismatches 4
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RESULT 12
HV3N_HMAN
ID HV3N_H
AC P01775
DT 21.JUL
DT 15-JUL
DT 15-JUL
DT SEWARY
OC MARMAI
OX NCBI_T
RN [1]
RP SEQUEN
RX MEDLIN
RX MEDLIN
RA Capra
RT anti-c
RT anti-c
RI PIC.
CC -!- MI
CC -!- MI
CC FIR; I
DR Pfam;
RW Inmunc
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HV3M_HUMAN
ID HV3M_HUMAN
AC P01774;
DT 21-JUL-1986
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Matches 14
GLOBULIN ACTIVITY.
PIR; A02058; M3HULY.
HSSP; P01772; 2IG2.
InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
                                                                                               Capra J.D., Kehoe J.M.; "Structure of antibodies with shared idiotypy: the complete of the heavy chain variable regions of two immunoglobulin M
                                                                   anti-gamma globulins.";
Proc. Natl. Acad. Sci. U.S.A.
-!- MISCELLANEOUS: THIS CHAIN
                                                                                                                              MEDLINE=75046755; PubMed=4139708; Capra J.D., Kehoe J.M.;
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-III REGION LAY.
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SEQUENCE
                                                                                                                                                        SEQUENCE
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PIR; A02057; M3HUPM.
HSSP; P01772; 2IG2.
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15-JUL-1999 (Rel. 38, Last s
IG HEAVY CHAIN V-III REGION
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Last annotation 
REGION POM.
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WAS ISOLATED FROM IGM WITH ANTI-GAMMA
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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21-JUL-1986.(Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MOPC 21 PRECURSOR (FRAGMENT).
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Immunoqlobulin V reg:
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Adetugbo K., Milstein C., Secher D
"Molecular analysis of spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies: somatic mu
Cell 24:625-637(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 265:299-304(1977).
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13; Conserv
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D SEGMENT.
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               J. Mol. Biol. 141:369-391
PIR; A02055; G1HUKL.
PDB; 2FB4; 12-JUL-89.
PDB; 2IG2; 12-JUL-89.
InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
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"Crystallographic refinement and
immunoglobulin molecule Kol and i
                                                                                                                                                                                                                                           Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies.
structure of crystallized monoclonal immunoglobulin IgG1
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                           SEQUENCE, AND DISULFIDE BONDS. MEDLINE=83289131; PubMed=6884994;
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence
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Immunoglobulin V region.
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Stoppini M., Bellotti V., Negri A.,
"Characterization of the two unique
Immunoglobulin
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ALIGNMENTS

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Query Match
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Q9UL91;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
Q9UL72 PRELIMINARY;
Q9UL72;
01-MAY-2000 (TrEMBLrel. 13,
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118 AA; 12843 MW;
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Q9ULB6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
IMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                "Human VH gene sequence.";
Submitted (NOV-1999) to the
EMBL; AB035268; BAA87067.1;
HSSP; P01772; 2FB4.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Van der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                         INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF035042; AA
HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTERPRO;
                                                                            2 LQLAESGGVLVQPGXSDRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LQLAESGGVLVQPGXSDRL 20
:|| ||| ||| ||| || || ||
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                                                                VQLEESGGGLVQPGGSLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                             VQLVESGGGLVQPGGSLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunol. Immunopathol. AF035042; AAD56278.1;
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 73.'
14; Conservative
                                                                                                                                                                                                     IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003006; -.
                                                                                                                                                            95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
118 AA;
               PRELIMINARY;
                                                                                                          Conservative
                                                                                                                                                                        95
2
                                                                                                                                                                                           ig; 1.
                                                                                                                                                           . 95
10527 MW;
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; 12872 MW;
                                                                                                                  65.68;
73.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%;
73.7%;
                                                                 19
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                                                                                                         1;
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                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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Pred. No. 0.01
1; Mismatches
               PRT;
                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87:184-192(1998).
                                                                                                                                                          90A8C6D16D22574A CRC64;
                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B4D1A5944B2D5CCA CRC64;
                                                                                                                   NO.
              113
                                                                                                                   DB 4;
0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
0.012;
              A
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                                                                                                                          Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 118
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                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                    Gaps
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Q9UL71
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POUL93

AC DO DE DE COMPENSOR RANGE EN COMPENSOR RA
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RESULT
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Best Local Similarity
Watches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                 Query Match
Best Local S
Matches 13
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UL93 PRELIMINARY; PRT; 116 AA.
Q9UL93;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035021; AAD56257.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                            PFAM; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                        fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR003006;
PFAM; PF00047; ig; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                        NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF035024; AAD56260.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etus.
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:|| |||| :|||| | ||
6
                                                                                     LQLAESGGVLVQPGXSDRL 20
                                                            VQLVESGGGVVQPGRSLRL
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                                                                                                                                            ch 63.4%;
l Similarity 68.4%;
l3; Conservative
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                                                                                                                                                                                                                                                                                                                                                   IPR003006; -.
                                                                                                                                                                                                                                                           116
116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 113
113 AA; 12437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ig; 1.
                                                                                                                                                                                                                                                    116
; 12434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    der Merwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.4%;
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                                                                                                                                            Score 59; DB
Pred. No. 0.03
2; Mismatches
                                                                                                                                               2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       0DA0348154DD6061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                 DB 4;
0.035;
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0.034;
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                                                                                                                                                                                    Length 116;
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                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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Q9UL71

PRELIMINARY;

PRT;

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Best Local S
Matches 13
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Best Local Similarity
Matches 13; Conser
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Q9UL84;
01-MAY-2000 (
01-MAY-2000 (
01-OCT-2000 (
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01-MAY-2000
01-MAY-2000
01-OCT-2000
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol
EMBL; AF035030; AAD56266.1;
HSSP; P01772; 2FB4.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol: Immunopathol. 87:184-192(1998)
EMBL; AF035043; AAD56279.1; .
HSSP; P01772; 2FB4.
INTERPRO; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                        PFAM;
                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                          INTERPRO;
                                                                                                                                                                                                                                                                                                                                      fetus."
                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young D.C
                                    N
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                                  LQLAESGGVLVQPGXSDRL 20
VQLVESGGGVVQPGRSLRL 20
                                                                                                                                                                                                                                    PRO; IPR003006; -. PF00047; 19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00047;
                                                                                                                                                                                                                                                                                                                  Immunol. Immunopathol.
                                                                                              Similarity
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121 AA;
                                                                                                                                                                          122
122 AA;
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , 19; 1.
1
                                                                                                                                                                                                                   ig; 1.
                                                                                                                                                                          122
13579 MW;
                                                                                                                                                                                                                                                                                                                                                                                              der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
13154 MW;
                                                                                            68.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.48;
                                                                                                                                                                                                                                                                                                                                                                                              Merwe
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                                                                         Score 59; DB
Pred. No. 0.03
2; Mismatches
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Pred.
                                                                                                                                                                                                                                                                                                              87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                            P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                            36054D41366545B8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalis
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                                                                                              DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                            N.N., Berney
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01-MAY-2000
01-MAY-2000
01-OCT-2000
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C. R. Acad. Sci., II
HSSP; P01789; IMCP.
SEQUENCE 15 AA; 1
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; Van der Merwe P.L.,
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Q9Y509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.

MEDLINE-95094032; PubMed-8000909;

Cohen H., Cohen O., Gagnon J.;

"Serum prolactin-binding protein (PRL-BP) of human
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10118;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation updat
prolaCTIN-BINDING PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                           ch 58.1%;
| Similarity 78.6%;
| Similarity 78.6%;
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13; Conservative
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Primates;
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Rodentia;
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2; Mismatches
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Pred. No. 0.02
1; Mismatches
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                              PRT;
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01-NOV-1999
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VH3 PROTEIN
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., William A.K.M., Misra S.;

Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;

Wilde K.G., William A.K.M., Misra S.;

Wilde K.G., William A.K.M., Misra S.;

Wilde K.G., William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K.M., Misra S.;

William A.K
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2000 (TrEMBLrel. 15,
GAMMAI HEAVY CHAIN OF MAB7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Mammalia; Eutheria;
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                                                                     VQLQESGGGLVKPGGSLKL
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| 12; Conser
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                                                                                                                                                                                                                                                                                    AA;
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Primates;
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63.2%;
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; Murinae; Mus
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; Homo.
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Matches
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CN 8:
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STRAIN=BALB/C; TISSUE=
Shinohara N., Demura T
Submitted (DEC-1999) t
                                                                                                                                                                                                                                                                                                                Q9X7E8;
Q9X7E8;
01-NOV-1999
                                                                                              James K.D.
Submitted
SEQUENCE FROM N.A.

MEDLINE=93188700; PubMed=8446027;

Eiglmeier K., Honore N., Woods S.A.,

"Use of an ordered cosmid library to
of Mycobacterium leprae.";

Mol. Microbiol. 7:197-206(1993).

EMBL; AL049478; CAB39580.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1999) to the EMBL; AB036341; BAA88633.1; HSSP; P01607: 1RFT
                                                                                                                                           MEDLINE=93188700; PubMed=8446027;
Seeger K.J., Harris D.;
"Use of an ordered cosmid library to
of Mycobacterium leprae.";
Submitted (MAR-1999) to the EMBL/GenE
                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-NAY-2000 (TrEMBLrel. 13, Last annotation
PUTATIVE PSEUDOURIDINE SYNTHASE.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Actinomycetales;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                      Mycobacterium leprae. Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody recognizing a
method.";
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"Isolation of a novel type of vascular cell wall-specific monoclonal recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                      SEQUENCE
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D., Parkhill
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Demura T., Fukuda
-1999) to the EMBI
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the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                              59
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                                                                                                                                              EMBL/GenBank/DDBJ
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Pred. No.
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Sciurognathi;
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Mismatches
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thi; Muridae;
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RESULT OCCUPANT REAL PROPERTY OCCUPANT 
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Best Local S
Matches 10
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Best Local Similarity
Matches 13; Conserv
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09UC53;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
77 KDA SPONTANEOUS RECURRENT ABORTION-ASSOCIATED HUMAN EMBRYONIC ANTIGEN/IGVHIII HOMOLOG (FRAGMENT).
MEDLINE-97298311; PubMed-9153759;
Jauniaux J.C., Poirey R.;
"Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV
reveals 26 open reading frames including SEC63, CDC31, SUG2, GCD1,
RBL2, PNT1, PAC1 and VPH1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
CHROMOSOME XV READING FRAME ORF YOR256C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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NCBI_TaxID=4932;
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Pred. No. 0.72
1; Mismatches
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PFAM; PF02225; PA; 1.
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EMBL; Z75164; CAA99478.1;
380 LLSRLSSGGVTVDDGNSDR
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10; Conser
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398
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                                          Score 45;
Pred. No.
                                                                               D7D68C0A8C50ECB2
                                    Mismatches
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58;
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                                                   Length 809;
                                                                               CRC64;
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Search completed: June 13, 2001, 14:29:44 Job time: 545 sec

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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 US-08-859-931A-4
US-08-545-809A-125
US-07-977-696C-75
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US-08-974-899-6
US-08-987-352B-11
US-08-9887-352B-11
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                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/859,931A FILING DATE: 21 MAY 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GOLTDON:
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7860
INFORMATION FOR SEQ ID NO: 4:
                                                                          Query Match
Best Local S
Matches 18
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LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTYWARE: PATENTIN RClease #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FASANO, Alessio TITLE OF INVENTION: SUBSTANTITLE OF INVENTION: PHYSIOI TITLE OF INVENTION: MAMMAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
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.4, Application US/08859931A
o. 5945510
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                                                                                             90.0%;
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US-09-619-491-10
PCT-US95-07302-10
US-07-942-245-38
US-07-942-245-38
US-08-545-809A-103
US-08-545-809A-103
US-08-545-809A-130
US-08-645-809A-130
US-08-645-809A-130
US-08-645-809A-130
US-08-645-809A-130
US-08-68-695-49
US-08-68-695-49
US-08-68-72-788A-23
US-08-472-788A-23
US-08-9858-201-2
                                                                          Score 80; DB Pred. No. 1.1e 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 75,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TELEX: 200154
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

FILING DATE: 27-MAR-100

PRIOR APPLICATION APPLICATION OF THE PRIOR A
                                                                                                                                             TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,0
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ceriani Dr., Roberto L.
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette
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ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-542-8906
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                                             STREET:
                                                                             ADDRESSEE:
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5792852
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SEE: PRETTY, SCHROEDER & POPLAWSKI : 444 South Flower Street, Suite 2000 Los Angeles
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Padlan Dr., Eduardo A.
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10-MAY-1993
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73.7%;
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SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
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Pred. No. 0.00
2; Mismatches
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RESULT 4
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPAILBLE

OPERATING SYSTEM: PC-DOS/MS-POS 5.0

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/129,930B

FILING DATE: September 30, 1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Amzel ph.D., Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: CRECC-008A
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Best Local Similarity
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6688
TELEPAX: (510) 748-6688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 11-16-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                         ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
                                                                                                                                                                                                                                                        COUNTRY: UZIP: 94596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 amino acids
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                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peterson Dr., Jerry A. Padlan Dr., Eduardo A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ceriani Dr., Roberto L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            do Couto Dr., Fernando J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                Analogue Peptides With Broad
Carcinoma Specificity, and Kit and
Diagnostic Vaccination and
Therapeutic Methods
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Pred. No. 0
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US-08-859-931A-2
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                                                                          Query Match
Best Local Similarity
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Best Local Similarity 73.7%;
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                                                                                                                                                                                                                                                  TELEFAX: (202) 293-7860 INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: PHY
TITLE OF INVENTION: MAM
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-9901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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                             LQLAESGGVLVQPGXSDRL 20
VQLVESGGGLVQPGGSLRL 20
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                                                                                                                                                                                    amino acid
3Y: linear
                                                                                                                                                                                                                   20 amino acids
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(510) 521-3541
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73.78;
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                                                          Score 62; DB
Pred. No. 0.00
1; Mismatches
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Pred. No.
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US-08-471-780C-80
; Sequence 80, Applicat
; Patent No. 5759808
; GENERAL INFORMATION:
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                                                                                                                                                         Sequence 80, Application US/08467282B Patent No. 5800988
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                             GENERAL INFORMATION:
APPLICANT: Casterman, Cecil
APPLICANT: Hamers, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: . 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
ORGANISM: Came
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 049
TELECOMMUNICATION INFORMATION:
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FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Hamers, Raymond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
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5759808
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1300 I Street, N.W.
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                                                                                                                     Casterman, Cecile
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Pred. No. 0.
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TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Cam
                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       APPLICANT: Casterman, Cecile APPLICANT: Hamers, Raymond
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS LENGTH: 26 amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-AUG-
APPLICATION NUMBER:
FILING DATE: 21-AUG-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
FILING DATE: 06-JUN-19
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                                                                                                                                                     COUNTRY:
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                 APPLICATION NUMBER:
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                                                                                                                                       20005-3315
                                                                                                                                                                                     Washington
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amino acid
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                                                                                                                                                     USA
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MBER: US/08/471,282A
06-JUN-1995
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73.7%;
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Pred. No. 0.001;
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                                                                                 PEILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
APPLICATION AUMBER: 17-AUG-1993
FR 92/
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APPLICATION NUMBER: FR 924
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
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TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                              FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 9:
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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                  APPLICATION NUMBER: FR 93401310.3 FILING DATE: 21-MAY-1993
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1300 I Street, N.W.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
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TOPOLOGY:

OLECULP

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OLECULP

OTHER TOPOLOGY:

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FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: POLLER, Jane E.R.
REGISTRATION NUMBER: 33,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
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MEDIUM TYPE: Floppy disk
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ORIGINAL SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 20005-3315
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1300 I Street, N.W.
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Pred. No. 0.001;
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Best Local Similarity
                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: CINFORMATION FOR SEQ ID NO: 17:
                                                                                                 TITLE OF INVENTION: Production of chimeric antibodies TITLE OF INVENTION: combinatorial approach NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                  APPLICANT: JESPERS, Laurent Stephane Anne Therese APPLICANT: WINTER, Gregory Paul
                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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 STREET: 6300 S
CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: TRUJILLO, DOREEN YATKO REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 06 JUI
                                                 ADDRESSEE:
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                                                                      ADDRESSEE:
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Illinois
                                 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                    \ensuremath{\mathsf{HOOGENBOOM}} , Hendricus Renerus Jacobus Matteus BAIER, Michael
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                     Borun
                                                               David W. Clough, Marshall O'Toole Gerstein Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
73.7%;
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Pred. No.
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Pred. No. 0
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               07-942-245-37
                                                                                                                                      TITLE OF INVENTION: SURTIFLE OF INVENTION: ANT NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                  tent No.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
                                                                                                                                                                                                                      APPLICANT: APPLICANT:
                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9 FILING DATE: 23-SEP-1991 PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                               CITY: Washington STATE: D.C.
                                                                 COUNTRY:
                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 15-MAY-1992
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                                                                                                                             DDRESSEE:
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FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 9120377.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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OGY: linear
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                                                                                                           E: Sughrue, Mion, Zinn, Macpeak & Seas 2100 Pensylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                               Application US/07942245
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GUILD,
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                                                                                                                                                                                                                                                 SEARLE,
                                                                 United States
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24-mar-1992
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Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES
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                                                                                                                                                                                                                                    Stephen M.J.
Anthony R.
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Pred. No.
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; TOPOLOGY: linear
; MOLECULE TYPE: pept
US-07-942-245-37
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Best Local (
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                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/65,202
FILING DATE: 13-UUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
                                                                                                                                                                                                                    FILING DATE: 14-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
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CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (202) 293-7060
                                                                                                                                                                                      FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                      NAME: HUNTER: TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
RELECOMMUNICATION INFORMATION:
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LENGTH: 98 amino acids
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APPLICATION NUMBER: US/07/942,245
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STREET: Tw
             STRANDEDNESS:
                                                                                                         TELEPHONE:
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                                            ENGTH:
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TELEX: 6491103
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5. 5977322
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                            amino acid
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                                            98 amino acids
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linear
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) 576-0300
NO: 31:
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73.7%;
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; FEATURE:
; NAME/KEY: F
; LOCATION: 1
US-08-428-197-4
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Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR ST.
TITLE OF INVENTION: VARIABLE REGI.
TITLE OF INVENTION: VARCINATION WITLE OF INVENTION: VARIABLE REGI.
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
    В
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US-08-428-197-4
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                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: PCT/US93/10555
APPLICATION UNBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOWells, Stacy L.
REGISTRATION UNDBER: FD-2630
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                      Query Match
Best Local S
Matches 14
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Best Local Similarity 73.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: SFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 90067
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2 VQLVESGGGLVQPGGSLRL 20
2 LQLAESGGVLVQPGXSDRL 20
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2 VQLVESGGGLVQPGGSLRL 20
                                                                                      Similarity 73.7
14; Conservative
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SILVERMAN, GREGG J.

VENTION: METHOD FOR STIMULATING PRODUCTION OF
VENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
VENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
                                                                                    66.7%; Score 62; DB 2; Length 108; 73.7%; Pred. No. 0.0048; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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Pred. No. 0.0043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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                                                                                    Gaps
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Search completed: June 13, 2001, 14:27:07 Job time: 628 sec

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq
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SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:

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SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:

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SIDS6/gcgdata/geneseq/geneseqp/AA1987.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1989.DAT:

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US01-05825A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLVESGGXL 11
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Compugen Ltd
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Pred. No. is the score greater than and is derived is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, ited by analysis of the total score distribution.

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| 20 | 20 | 18 | : 11 | 11 | 150 | 119 | 100 | Query Match Length DB |
| 21 | 19 20 | 19 | 21 | 20 | 20 | 16 | 21 | DB. |
| Y84660 Y79130 | W68169 | W73953 W68167 | Y79134 | W94492 | Y07484 | R66308 | B40083 | ID |
| N-terminal sequenc Human adult heart | Human IgG heavy ch Human adult heart | IgG heavy chain fr Complex scuPA/suPA | Human adult intest | Human adult intest | Anti-HIV-1 gp120 a | Human immunoglobul | Ø | Description |

| 45 | 44 | 3 | 42 | 1 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
|--------|---------|--------|------------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------|--------|----------|--------|--------|---------|--------|--------------------------|------------|----------|--------|--------|--------|-----------|--------------------|--------|--------------------|
| | | | | 4 | 4 | | | | | | | | | | | 46 | | | | | | | | | | | | | | | | | |
| 5 | Ġ | Ü | Ġ | Š | Ġ | 5 | ÿ | 5 | Ġ | 5 | 5 | Š | 5 | ú | <u>5</u> | | 5 | 5 | 5 | 5 | | 5 | ŗ | <u>5</u> | 5 | <u>ب</u> | 5 | ŗ | • | <u>ب</u> | 5. | 5 | 5 |
| 100 | 0 | 99 | 98 | . 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 98 | 97 | 97 | 96 | 85 | 89 | 30 |
| 17 | 17 | 21 | 22 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 21 | 19 | 16 | 15 | 14 | 21 | 21 | 21 | 21 | 21 | 17 |
| R96106 | R96105 | Y50960 | B48022 | Y56660 | Y50964 | B40140 | B40139 | B40138 | B40137 | B40136 | B40134 | B40133 | B40131 | B40130 | B40113 | в40096 | в40095 | B40094 | B40087 . | B40086 | B40085 | B40084 | B40072 | W59614 | R72074 | R52066 | R34279 | B40132 | B40112 | Y56646 | Y64735 | B53646 | R87049 |
| -15 | 5 autoa | FVIII | chain sequ | | Η | Anti-hIL12 antibod | -hIL12 | N | | -hIL12 | -hIL12 | -hIL12 | -hIL12 | N | Anti-hIL12 antibod | N | | | -hIL12 | -hIL12 | -h1L12 | i-hIL12 | -hIL12 | <pre>-RSV F protei</pre> | 'H region. | cha | an | hIL1: | -hIL1 | ial pepti | Human 5' EST relat | olon c | Human group III he |

ALIGNMENTS

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RESULT
B40083
в40083;
                                                                                     Anti-hIL12 antibody H chain V region amino acid sequence
                                                                                            05-FEB-2001 (first entry)
                                                                                                          B40083 standard; Protein; 100
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SEQ ID 609.

Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory; complementarity determining region; CDR; antirheumatic; antiarthritic; antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis.

Homo sapiens.

WO200056772-A1. 28-SEP-2000

24-MAR-2000; 2000WO-US07946

25-MAR-1999; 99US-0126603

(BADI) BASF AG. (GEMY) GENETICS INST INC.

Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A; Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR; Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL; White M;

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DT PT T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
R66308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a new human antibody specific for human content of interleukin-12 (IL-12). The invention also includes antigen binding that bind to IL-12. Sequences B39485-B39516 represent human compared to the property of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
DNA fragment comprising human immunoglobulin Vh production of human immunoglobulin in mammalian
                                                                      WPI; 1995-006791/01
N-PSDB; Q78953.
                                                                                                                                      Honjo T,
                                                                                                                                                                                                                     10-MAY-1993;
                                                                                                                                                                                                                                                             10-MAY-1993;
                                                                                                                                                                            (NISB ) JAPAN TOBACCO
                                                                                                                                                                                                                                                                                                       24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R66308 standard; Protein; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R66308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin variable heavy chain #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-638250/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity 90.1
                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; amplify; human; immunoglobulin; variable; heavy chain; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                    Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 121; 377pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA;
                                                                                                                                                                                                                 93WO-JP00603.
                                                                                                                                                                                                                                                           93WO-JP00603.
                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB
Pred. No. 0.12
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Length 100,
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  genes
hosts
                   for
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XX PN XX
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Y07484
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Best Local S
Matches 10
This sequence represents the heavy chain variable region of the human anti-HIV-1 gp120 monoclonal antibody 447-D. The antibody is targeted to an epitope on the V3 loop of gp120. The invention relates to the generation of heterohybridomas producing human monoclonal antibodies
                                                                                                                                                                                                                                       23-APR-1992;
15-JUN-1990;
12-APR-1991;
21-NOV-1994;
                                                                            Claim
                                                                                                          Heterohybridoma producing human monoclonal antibodies
                                                                                                                                           WPI; 1999-370481/31.
N-PSDB; X79205.
                                                                                                                                                                                    Gorny MK,
                                                                                                    immunodeficiency
                                                                                                                                                                                                            (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                        21-NOV-1994;
                                                                                                                                                                                                                                                                                                                                   22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                            US5914109-A
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                epitope; V3 loop
peripheral blood
                                                                                                                                                                                                                                                                                                                                                                                                                       Heavy chain; variable region; human; HIV-1; gpl20; epitope; V3 loop; heterohybridoma; human immunodefj
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-HIV-1 gp120 antibody 447-D VH chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences encoded by novel isolated genes. The genes (Q78939-79002) were v6;Y24; 3-31; M84; M118 and M131, by PCR amplification using primers (Q78917-38. The genes are subdivided into 5 families of Vh genes. The high molecular weight DNA from human placenta. The DNA was partially gel electophoresis and 35-45 kb fraction swere collected. The fragments were in vitro packed and infected into 5 families of Wh genes. The products were in vitro packed and infected in the DNA fragments were sparated by the electophoresis and 35-45 kb fractions were collected. The fragments products were in vitro packed and infected into E.coli 490A. The DNA fragments were then subcloned by colony hybridisation. The Vh genes and immunoglobulin in mammalian hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y07484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y07484 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein sequences sequences encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 24; Page 49-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLVESGGXL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
10; Conserv
                                                                       Fig 11; 42pp; English.
                                                                                                                                                                                 Zolla-Pazner S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                    92US-0872675.
90US-0538451.
91US-0684090.
94US-0345321.
                                                                                                                                                                                                                                                                                                       94US-0345321
                                                                                                   virus-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (R66295-51) are novel human immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            Epstein-Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      human immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                         virus; EBV; AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody;
                                                                                                             to humar
                                                                                                                                                                                                                                                                                                                                                                                                                      virus-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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RESULT
W94492
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   The present invention describes pure zonulin which has an apparent CC molecular weight of 47 kD, as determined by SDS-PAGE, which is CC recognised by both anti-tau polycional antibody and by anti-zonula CC occludens toxin (20T) polycional antibody, and is capable of reversibly CC opening mammalian tight junctions. Zonulin proteins function as CC physiological modulators of mammalian tight junctions. They can be used CC for enhancing the absorption of therapeutic agents across tight CC junctions of intestinal and nasal mucosa and across tight junctions of the blood brain barrier. Zonulin can be used with agents such as drugs, CC e.g. lidocaine, adenosine, dobutamine, dopamine, epinephrine, cc correpinephrine, phentolamine, doxapram, alfentanil, dezocin, nalbuphine, CC uncrepinephrine, naloxone, ketorolac, midazolam, propofol, metacurine, CC uncristine, vinblastine, methicillin, mezlocillin, piperacillin, CC cetoxitin, cefenicid, cefmetazole and aztreonam, a hormone e.g. CC testosterone, nandrolene, menotropins, insulin, urofolltropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                        New purified zonulin - which is capable of reversibly opening mammalian tight junctions, used for enhancing the delivery of agents across intestinal and nasal mucosa and blood brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to a neutralising epitope of human immunodeficiency virus-1 (HIV-1) prepared by transforming peripheral blood lymphocytes with Epstein-Barr virus. The antibodies can be used to treat someone infected with HIV-1
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-070123/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zonulin; mammalian tight junction; zonula occludens toxin; ZC Vibrio cholerae; vaccine; cholera toxin; polyclonal antibody: intestinal mucosa; nasal mucosa; blood brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adult intestine zonulin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W94492 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or suffering from AIDS
                                                                                                                                                                                                                                                                           Example 3; Fig 6; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide;
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Pred. No. 0.
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Best Local S
Matches 11
                                   The present sequence is that of the N-terminal region of adult human intestinal zonulin. The N-terminal sequences of human adult and foetal zonulins (see Y79130-36) were compared with vibrio cholera zonula occludens toxin (ZOT) to identify a common motif thought to be involved in receptor binding. Peptide antagonists (see Y79105-29) based on this motif are useful as antiinflammatory agents for treatment of gastrointestinal inflammation, and for treatment of conditions associated with breakdown of the blood-brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon-alpha, interferon-beta, interferon-gamma, interleukin-1 (IL-1), IL-2, IL-4, IL-8, polyvalent IgG, specific IgG, IgA, or IgM. The proteins can also be used for the production of antibodies which can be used to assay for zonulin in body tissue or fluids, or in affinity-purification of zonulin. The present sequence represents a zonulin
                                                                                                                                                                                 New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zonulin; antagonist; zonula occludens toxin receptor; human; blood-brain barrier; antiinflammatory; gastrointestinal inflammation; therapy.
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Sequence
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                                                                                                                                                                                                                                                                                                                     03-AUG-1998;
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                                                                                                                                                         Example 3; Fig 6;
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                                                                                                                                                                                                                                                                                          MARYLAND BALTIMORE
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "unidentified residue"
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100.0%; Pr
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                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal sequence
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0.016;
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Best Local Similarity
Matches 11; Conserva

Conservative

Pred. No. 0.016; Mismatches 0;

Indels

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RESULT
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                                                                                                                            Matches
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                  This sequence represents a fragment of the IgG heavy chain. This sequence was isolated using the biomedical device of the invention, which comprises: (a) a biocompatible support; and (b) conglution, which is covalently bound to the support. The device can be used for removing immune complexes (IC) from a fluid. This can be used for treating a mammal or for evaluating the status of a mammal. It can be used for treating diseases such as serum sickness, chronic immune complex nephritis, bacterial infections, viral infections, parasitic diseases, autoimmune diseases or neoplastic diseases. The devices can also be used for purification of IC and to study immune pathogenesis and antigens associated with a disease state. The covalently immobilised conglutinin can capture IC with high capacity and specificity and allows elution under mild conditions. The devices are stable with no loss of IC binding
W68167 standard;
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New biomedical device for binding immune complexes - comprising conglutinin covalently bound to a solid phase material
                                                                                                                                                                                                                            activity after repeated use.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Fig 11; 58pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-106945/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMU-) APPLIED IMMUNE SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IgG heavy chain; immune complex removal; conglutinin; infection; serum sickness; chronic immune complex nephritis; parasitic disease; autoimmune disease; neoplastic disease; immune pathogenesis; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09506254-A1
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                                                                                                                                         Similarity
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                                                                                                                            Conservative
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peptide;
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                                                                                                                                        95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okarma TB;
 18
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                                                                                                                                       Score 46;
Pred. No.
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                                                                                                                                                    DB 16; Length 18;
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RESULT
W68169
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                                                                                                                                                                                                                                            This represents a human immunoglobulin G (IgG) derived peptide sequence that has a stimulating effect on the fibrinolytic activity of the scuPA/CC suPAR complex of the invention. This sequence has similarity to the human IG heavy chain, IG V-III region (HV3T). The invention provides a CC thrombolytic therapeutic composition for the treatment and prevention of a thromboembolic disorder associated with the formation of fibrin clots. CC The composition comprises, as the active ingredient, a complex of a CC single chain urokinase type plasminogen activator (scuPA) and a soluble CC urokinase plasminogen activator receptor (suPAR). The complex (scuPA/CC suPAR) has thrombolytic activity under physiological conditions and in CC the presence of IgG, or of at least 1 IgG-derived peptide, and induces CC the presence of fibrin clots. The compositions and complex are useful CC the presence of fibrin clots. The compositions and complex are useful CC with the formation of fibrin clots, especially myocardial infractions, CC cerebro-vascular events, pulmonary embolism and deep vein thrombosis.
                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                        Matches
 W68169 standard;
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compositions with thrombolytic activity for, e.g. treatment of thromboembolism - comprise complex of single chain urokinase type plasminogen activator, scuPA, and soluble urokinase plasminogen activator scuPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombolytic activity; soluble urokinase plasminogen activator receptor; single chain urokinase type plasminogen activator; thromboembolism; scuPA; suPAR; 19[5] regulator; fibrinolytic activity; fibrin clot; myocardial infraction; cerebro-vascular event; pulmonary embolism; deep vein thrombosis; immunoglobulin; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 24; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-348262/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Higazi AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complex scuPA/suPAR fibrinolytic activity regulating
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peptide;
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                                                                                                                                                                     100.0%;
                                                                                                                                                                     95.8%; Score 46; 100.0%; Pred. No.
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                                                                                                                                                                     DB 19;
0.028;
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RESULT
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AC WS
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AC Ho
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                                                                                                                                                                                                                                                                                                                                                                           the formation of fibrin clots. The composition comprises, as the active ingredient, a complex of a single chain urokinase type plasminogen activator (scuPA) and a soluble urokinase plasminogen activator receptor (suPAR). The complex (scuPA/suPAR) has thrombolytic activity under physiological conditions and in the presence of IgG, or of at least 1 IgG-derived peptide, and induces fibrinolysis of fibrin clots. The compositions and complex are useful for the treatment or prevention of thromboembolic disorders associated with the formation of fibrin clots, especially myocardial infractions, cerebro-vascular events, pulmonary embolism and deep vein thrombosis.
Human adult heart zonulin N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This represents a peptide sequence from the human immunoglobulin G (IGG) heavy chain, IG V-III region (HV3T). An IGG derived peptide sequence having similarity to this sequence has a stimulating effect of the fibrinolytic activity of the scuPA/suPAR complex of the invention. The invention provides a thrombolytic therapeutic composition for the treatment and prevention of a thromboembolic disorder associated with the treatment and prevention of a thromboembolic disorder associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compositions with thrombolytic activity for, e.g. treatment of thromboembolism - comprise complex of single chain urokinase type plasminogen activator, scuPA, and soluble urokinase plasminogen activator scuPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single chain urokinase type plasminogen activator; thromboembolism; scuPA; suPAR; IgG; regulator; fibrinolytic activity; fibrin clot; myocardial infraction; cerebro-vascular event; pulmonary embolism; deep vein thrombosis; immunoglobulin; human.
                                                                                                     W94487 standard;
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                                     21-APR-1999
                                                                                                                                                                                                                                                                                                                                              Sequence
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                                   (first entry)
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                                                                                                       peptide;
                                                                                                                                                                                                                                                                           95.8%;
                                                                                                       20 AA
                                                                                                                                                                                                                                                                           Score 46; DB 19; Length 20; Pred. No. 0.032;
                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 10
Human; Zot; zonula occludens toxin; zonulin; antigen presenting cell;
                                N-terminal sequence of a human zonulin protein of 47 kDa
                                                                                                                                                                                                                                                                                                                                                                             Sequence
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CC recognised by both anti-tau polycional antibody and is capable of reversibly co-coludens toxin (207) polycional antibody, and is capable of reversibly co-pening mammalian tight junctions. Zonulin proteins function as co-coludens toxin (207) polycional antibody, and is capable of reversibly co-pening mammalian tight junctions. They can be used co-colleged the bloody and modulators of mammalian tight junctions. They can be used co-colleged the blood brain barrier. Zonulin can be used with agents such as drugs, co-colleged the blood brain barrier. Zonulin can be used with agents such as drugs, co-colleged the blood brain barrier. Zonulin can be used with agents such as drugs, co-colleged the proportion, phentolamine, doxapram, alfentanil, dezocin, nalbuphine, co-colleged the proportion, nalouphine, co-colleged the proportion, succinylcholine, cytarabine, mitomycin doxorubicin, co-colleged the proportion, methicilin, mezlocillin, piperacillin, co-colleged the colleged to assay for zonulin in body tissue or fluids, or in affinity-colleged to assay for zonulin in body tissue or fluids, or in affinity-contention of zonulin. The present sequence represents an N-terminal contention of zonulin. The present sequence represents an N-terminal contention of zonulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 45; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New purified zonulin - which is capable of reversibly opening mammalian tight junctions, used for enhancing the delivery of across intestinal and nasal mucosa and blood brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zonulin; mammalian tight junction; zonula occludens toxin; ZOT; Vibrio cholerae; vaccine; cholera toxin; polyclonal antibody; intestinal mucosa; nasal mucosa; blood brain barrier.
   25-JUL-2000
                                                                                                                                               Y84660 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes pure zonulin which has an apparent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-070123/06
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 47 kD, as determined by SDS-PAGE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 20; Pred. No. 0.032; 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
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organ transplantation; inflammatory disease; allergic disease; rheumatoid arthritis; insulin dependent diabetes mellitus; celiac disease; Sjogren's syndrome; systemic lupus erythematosus; auto-immune thyroidditis; iddopathic thrombocytopenic purpura; hemolytic anemia; Grave's disease; Addison disease; autoimmune orchitis;

APC; lymphocyte proliferation; antigen; auto-immune disorder; immune-related disorder; immune system rejection; multiple so

immune system rejection; multiple sclerosis;

pernicious anemia; vasculitis; autoimmune coagulopathy; polymyositis; myasthenia gravis; polyneuritis; pemphigus; rheumatic carditis; bermatomyositis; scleroderma; asthma; psoriasis; eczematous dermatitis; Karposi's sarcoma; inflammatory bowel disease; prollferative disorder.

Homo sapiens

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                                                Query Match
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Matches 11
                                                                                                                                                                                                                                       method can be used to down-regulate APC-mediated lymphocyte proliferation in mammalian hosts suffering from auto-immune or immune-related disorders, immune system rejection subsequent to tissue or organ disorders, immune related disorders include multiple sclerosis, rheumatoid or immune related disorders include multiple sclerosis, rheumatoid arthritis, insulin dependent diabetes melitius, celiac disease, syndrome, systemic lupus erythematosus, auto-immune thyroiditis, idiopathic thrombocytopenic purpura, hemolytic anemia, grave's disease, Addison disease, autoimmune orchitis, pernicious anemia, vasculitis, autoimmune coagulopathies, menoratis, pernicious anemia, vasculitis, autoimmune coagulopathies, myasthenia gravis, polyneuritis, penphigus, rheumatic carditis, polymyositis, and scleroderma. The inflammatory or allergic disease or disorder is selected from asthma, poorlassis, eczematous dermatitis, multiple sclerosis inflammatory bowal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the N-terminal of a human zonulin polypeptide. The specification describes a method of suppressing antigen presenting cell (APC)-mediated lymphocyte proliferation in a mammalian host pre-exposed to a particular antigen. The method comprises administering to the host an effective amount of a zot-related immunoregulator selected from Zot (zonula occludens toxin) or zonulin, the amount effective to down-regulate the activity of the APC. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suppression of antigen presenting cell mediated lymphocyte proliferation, by administering a Zot-related immunoregulator useful for treating immune-related disorders, immune system rejection subsequent to tissue or organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-271257/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 26; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                       Karposi's sarcoma, multiple sclerosis, inflammatory bowel disease, proliferative disorders of smooth muscle cells, and inflammatory conditions associated with mycotic, viral, parasitic, or bacterial
                                                                                                                                   Sequence
EVQLVESGGXL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Sztein MB,
                                                                    Similarity
                                                ilarity 100.0%;
Conservative (
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                                                                      95.8%; Score 46; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y79130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to be involved in receptor binding. Peptide antagonists (see Y79105-29) based on this motif are useful as antiinflammatory agents for treatment of gastrointestinal inflammation, and for treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions associated with breakdown of the blood treatment of conditions as the blood treatment of condit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of the N-terminal region of adult human heart zonulin. The N-terminal sequences of human adult ar foetal zonulins (see Y79130-36) were compared with Vibrio choles zonula occludens toxin (ZOT) to identify a common motif thought
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-205565/18
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Humanised antibody; interleukin-5; IL-5; recombinant antibody; antibody engineering; monoclonal antibody; MAb; 39D10; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       barrier.
                                                                           Human group III heavy chain framework 1.
                                                                                                                                                                                         R87049;
                                                                                                                                      25-JUN-1996
                                                                                                                                                                                                                                           R87049 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
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                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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0.032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody heavy chain showed homology to corresponding regions (R87053-56, respectively) of the rat anti-human interleukin-5 monoclonal antibody 39D10 heavy chain (see R87039). This homology was utilised in the prodn. of a humanised 39D10 VH (R87058) in which rat 39D10 VH complementarity determining regions were grafted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementarity determining region; heavy chain; framework; eosinophilia; allergy; asthma.
                                         08-MAR-2000; 2000WO-US05883
                                                                                                WO200055351-A1
                                                                                                                            Homo sapiens.
                                                                                                                                                      reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                                                                                                                 neural disorder; immune system disorder; muscular disorder;
                                                                                                                                                                                             immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antilnfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                        Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulne
                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                              09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                     B53646 standard; Protein; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Framework regions (R87049-52) of human group III (gp3) germ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-human IL-5 recombinant antibody - reducing eosinophilia and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-058412/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-1994;
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               12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CLLT ) CELLTECH THERAPEUTICS LTD
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                                                                                                                                                                                                                                                                  colon cancer antigen protein sequence SEQ ID
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               99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            framework.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementarity determining regions were grafted
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17; Length 30; 0.049;
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                                                                                                                                                                                                                                                                  NO:1186
                                                                                                                                                                                                                        vulnerary;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. C98764 to C98772 and B54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C97991 to C98763 encode the human colon cancer associated proteins called human colon cancer antigens, given in B53234 to B54006. The colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1766; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
WPI; 2000-038446/03
                          Dumas Milne Edwards J,
                                                                                 09-APR-1998;
28-APR-1998;
                                                                                                                          09-APR-1999;
                                                                                                                                                                                                                                                                                                       Human 5'
                                                                                                                                                                                                                                                                                                                                      01-FEB-2000
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                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                       regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
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nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 85
                                                                                                                                                                                                                                                                                                         EST related polypeptide SEQ ID NO:896.
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98US-0069047
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90.9%;
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Pred. No.
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Length 68; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc sequences, corresponding to human secreted proteins. Y64651 to Y65438 cc represent the EST-related proteins corresponding to Z4265 to Z43052. cc rhey can be used for producing secreted human gene products. cc rhey can be used for producing secreted human gene products. cc and upstream regulatory regions which control the location, development cc stage, rate, and quantity of protein synthesis, as well as stability of cc mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing cc extracellular secretion of a polypeptide or the insertion of a cc polypeptide into a membrane, or importing a polypeptide into a cell. cc The proteins encoded by the EST sequences may be useful in treating a cc variety of human conditions. Secreted proteins have therapeutic value, cc and the identification of new secreted proteins is valuable. 242249 to cc exemplification of the present invention.
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Y56646
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                               Complementarity determining region; antibody; primate; immunogenicity; old World ape; Old World monkey; antigen-binding affinity.
                                                                                                                                                                                                                                                                                                                                                                                              Partial peptide fragment of chimpanzee VH cDNA clone 41-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y56646 standard; protein; 96 AA.
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Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity humans -
                                                               WPI; 2000-023265/02.
N-PSDB; Z39314.
                                                                                                                                                                                                                  28-APR-1999;
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                                                                                                                                                                                                                                                                                                                Pan troglodytes.
                                                                                                                                                                                  28-APR-1998;
                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                  (complementarity determining regions) derived from a non-human antigen-specific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDBs from a non-human antigen-specific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                     The invention provides an antibody (Ab)
                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 54; 123pp; English.
                                                                                                                                                                                                       antibody.
1 evqlvesgggl 11
                                     1 EVQLVESGGXL 11
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Pred. No. 0.18;
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Result No.

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| 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 |
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| G1HUTE | S69132 | S31121 . | S31109 | S21980 | S34012 | S36259 | A34964 | S17079 | S78486 | HVMS34 | B28966 | S17080 | S21979 | S31668 | мзнист |
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Ig heavy chain V region (clone 17s.93) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1010
R;Tillman, D.M.: Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Accession: PH1010
A;Accession: PH1010
   A;Gene: GDB:IGHV@ ...

A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14932.33-14932.33
C;Superfamily: immunoglobulin V region; immu C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IM
F;22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A02061
R;Capra, J.D.; Kehoe, J.M.
Proc. Natl. Acad. Sci. U.S.A. 71, 845-848, 1974
A;Title: Variable region sequences of five human immunoglobulin heavy chain: A;Reference number: A93794; MUID:74142702
A;Accession: A02061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-116 < CAP>
                                                                                                                                                                                                                                    C; Comment: This chain was isolated from an IgAl myeloma protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-III region (Zap) - human (tentative sequence)
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RESULT 3
$21205
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #te
C;Accession: $21205
R;Maklya, R.; Stigbrand, T.
Eur. J. Biochem. 205, 341-345, 1992
Eur. J. Placental alkaline phosphatase has a binding
                              Ig heavy chain V region (YAC-5) - human C:Species: Homo sapiens (man) C:Decies: Homo sapiens (man) C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999 C:Accession: 946462 #sequence_revision 20-Feb-1995 #sequence
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S46462
      R;Cook, G.P.;
Nature Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo saplens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tomilnson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. MOI. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty
A:Reference number: S26885; MUID:93021117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-97 < TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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Bur. J. Blochem. 205, 341-345, 1992
A;Title: Placental alkaline phosphatase has a A; Reference number: S21205; MUID:92209522
A; Accession: S21205
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
C; Keywords:
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Best Local Similarity 90.0
Matches 10; Conservative
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7, 1
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nlinson, I.M.;
162-168, 1994
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90.98;
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                  Walter, G.;
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Pred. No.
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Pred. No. 0.00
0; Mismatches
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Pred. No.
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            Riethman,
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0.051;
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.039;
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         H.; Carter,
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      N.P.;
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   Buluwela,
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Wil
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A;Title: Continuing rearrangement but absence of somatic hypermutation in A;Reference number: PL0116; MUID:88286083
A;Recession: PL0121
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Nolecule type: mRNA
A;Residues: 1-98 <BIR>
A;Note: the sequence: B cells from patient TD with acute lymphoblastic C;Superfamily: immunoglobulin vegion; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>
F;15-98/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                           R;Bird, J.; Galili, N.; Link, M.; Stites, J. Exp. Med. 168, 229-245, 1988
                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V-III region (TD-Vp) - human (fragment) C;Species: Homo sapiens (man) C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type; mRNA
A; Residues: 1-98 <LEV>
A; Experimental source: strain BALB/cJ
A; Note: this sequence belongs to the VH7183 subfamily
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Reywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
F; 22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                C; Accession: PL0121
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PL0121
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A;Reference number: $46460; M
A;Accession: $46462
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <COO>
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A;Title: Early onset of somatic mutation in immunoglobulin VH A;Reference number: JT0501; MUID:89279149
A;Accession: JT0501
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If heavy chain V region (6.96) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30 Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
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Best Local
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Best Local Similarity 90.3
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Pred. No. 0.05
0; Mismatches
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Pred. No. 0.
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Ig heavy chain V-III region (TD-Vr) - human (fragment)
C;Specles: Homo saplens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0123; S26897
C;Accession: PL0123; S26897
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A;Reference number: PL0116; MUID:88286083
A;Accession: PL0123
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Residues: 1-98 <BIR>
A;Residues: 1-98 <BIR>
A;Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement fR;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of VA;Reference number: S26885; MUID:93021117
A;Steries on: S26885; MUID:93021117
                                                                                               Ig heavy chain v region (DP-53) - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: 526896
C:Accession: 526896
C:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups (A; Reference number: $26885; MUID:93021117
A; Reference number: $26885; MUID:93021117
A; Molecule type: DNA
A; Residues: 1-98 <TON>
A; Residues: 1-98 <TON>
A; Cross-references: EMBL:212353
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology <IMM>
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A;Rolecule type: DNA
A;Residues: 1-98 <TONA
A;Residues: 1-98 <TONA
A;Cross-references: EMBL:212354; NID:g32930; PIDN:CAA78224.1; PID:g32931
A;Cross-references: EMBL:212354; NID:g32930; PIDN:CAA78224.1; PID:g32931
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;J5-98/Domain: immunoglobulin homology <IMM>
F;J1-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2
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10; Conservative
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10; Conservative
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                     95.8%;
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Ig heavy chain V region (COS 6) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29545
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29543
A;Accession: S29543
A;Accession: S29543
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z17392; NID:g32840; PIDN:CAA78996.1; PID:g32841
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <TMM>
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(;Species: Homo sapiens (man)
(;C;Species: Homo sapiens (man)
(;C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
(;Accession: S26927
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fift: A;Reference number: S26885; MUID:93021117
A;Accession: S26927
C;Accession: S26932
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Moll. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885; MUID:93021117
A;Accession: S26932
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                                                                                                                                                                 Ig heavy chain V region (DP-39) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A; Residues: 1-98 <TOM>
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Pred. No. 0.052;
0; Mismatches
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Pred. No. 0.052;
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A;Cross-references: EMBL:Z14073; NID:g32973; PIDN:CAA78453.1; PID:g32974
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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c;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
c;Accession: S26940
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117
A;Accession: S26940
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A; Residues: 1-98 < TOM>
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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Pred. No. 0.052;
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C:Accession: S26894
Search completed: June 13, Job time: 743 sec
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (DP-51) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-98 < TOM>
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InterPro; IPR003006; -
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Immunoglobulin V region.
NON_TER 114 114
           p19181;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1990 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 HEAVY CHAIN V RECION 5A PRECURSOR.
Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cyprinidae; Cyprinidae; Cyprininae; Carassius.
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Canis familiaris (Dog).
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InterPro; IPR003006; -.
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Immunoglobulin V region.
NON_TER 98 98
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Biochemistry 16:3160-3168(1977);
--- MISCELLANEOUS: THIS CHAIN WA
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Mammalia; Eutheria; Carnivora;
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J. Exp. Med. 169:2007-2019(1989).
1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO
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ID HV3T_HUMAN STANDARD; PRT; 116 AA.

CC P01781;

VC P01781;

VI 21-JUL-1986 (Rel. 01, Created)

VI 21-JUL-1986 (Rel. 01, Last sequence update)

VI 15-JUL-1999 (Rel. 38, Last annotation update)

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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MEDLINE-88144476; PubMed-3125551;
Wilson M.R., Middleton D., Warr G.W.;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable region gene evolution:
"Interval and a pseudogene in a
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MU CHAIN WAS ISOLATED FROM
          Score 46; DB
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0; Mismatches
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
BY SIMILARITY.
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Pred. No. 0.01
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                                                                                                         2C67CA9AAAAA1282 CRC64;
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0.012;
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RESULT 6
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Best Local S
Matches 10
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980419; PRO419; (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence up

15-JUL-1999 (Rel. 38, Last annotation

IG HADY CHAIN V-III REGION GAR.
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P18526;
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01-NOV-1990 (Rel. 16, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V REGION 345 PRECURSOR.
                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
             InterPro; IPR003006; -. Pfam; PF00047; ig; 1. Immunoglobulin V region
                                                                   "Characterization of the two unique immunoglobulins."; Eur. J. Blochem. 228:886-893(1995). HSSP: P01810; 2FBJ.
                                                                                                                                                                  MEDLINE-95255298;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                  Stoppini M.,
                                                                                                                                                                                        SEQUENCE.
                                                                                                                                                                                                                         NCBI_TaxID=9606;
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10; Conser
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                                                                                                                                                5298; PubMed=7737190;
Bellotti V., Negri A
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tation in
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
BY SIMILARITY.
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Sciurognathi;
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human anti-flavin mono
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th1; Muridae;
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VH genes
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; Murinae; Mus
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monoclonal
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RESULT 8
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              MEDLINE-77117674; PubMed-65324; Capra J.D., Hopper J.E.; "Comparative studies on monotypic IgM individual patient. III. The complete region of the IgM paraprotein."; Immunochemistry 13:995-999(1976).
                                                                                                                                                                                                                                                 -W3E_HUMAN STANDARD; PR
P01766;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last seque
15-JUL-1999 (Rel. 38, Last annot
IG HEAVY CHAIN V-III REGION BRO.
                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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Immunoglobulin V region.
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SEQUENCE 119 AA; 1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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21-JUL-1986 (Rel. 01, Last s
15-JUL-1999 (Rel. 38, Last a
IG HEAVY CHAIN V-III REGION
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21-JUL-1986
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HSSP; P01772; 2IG2.
InterPro; IPR003006;
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Immunoglobulin V region.
NON_TER 120 120
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"Amino acid sequence of the heavy-chain variable region
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V-III REGION DOB.
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(Rel. 02, Last sequence update)
(Rel. 38, Last annotation update)
AIN V REGION G4 PRECURSOR.
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Pred. No.
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Best Local S
Matches 8
Wang A.-C., Wang I.Y., Fudenberg H.H.;
"Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977).
-!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
                                                                                                                                                         MEDLINE=78005528; PubMed=409716;
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P01765;
                                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                  Homo sapiens (Human), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo, NCBI_TaxID=9606;
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15-JUL-1999 (Rel. 38, Last annot
IG HEAVY CHAIN V-III REGION TIL.
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InterPro; IPR003006; -
Pfam; PF00047; ig; 1.
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Proc. Natl. Acad. Sci. U.S.A. 82:844-848(1985).
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Calman crocodilus (Spectacled caiman) (Caiman scla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat.
Archosauria; Crocodylidae; Alligatorinae; Caiman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide sequences of three VH genes in Caiman, a phylogenetically ancient reptile: evolutionary diversification coding segments and variation in the structure and organization
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InterPro; IPR003006; -.
Pfam; PF00047; 19; 1.
Immanoglobulin v region.
NON_TER 115 115
SEQUENCE 115 AA; 12356 M
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NON_TER 115 115
SEQUENCE 115 AA; 12379 M
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15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V-III REGION JON.
HOMO sapiens (Human).
EUKaryota: Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torano A., Putnam F.W.;

"Complete amino acid sequence of the alpha 2 heav
IGA2 immunoglobulin of the A2m (2) allotype.";

Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).

-I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, P
Capra J.D., Kehoe J.M.;
"Variable region sequences of five human immunoglobulin heavy
of the VH3 subgroup: definitive identification of four heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.. SEQUENCE.. PubMed-416441;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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IG HEAVY CHAIN V-III REGION BUT.
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                                                           MEDLINE=74142702; PubMed=4522793; Capra J.D., Kehoe J.M.;
                                                                                                          SEQUENCE
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InterPro; IPR03006; -.
Pfam; PF00047; 19; 1.
Immunoglobulin V region.
NON_TER 115 115
SEQUENCE '115 AA; 12563
                                                                                           InterPro: IPR003006; -. Pfam; PF00047; 1g; 1. Immunoglobulin v region. NON_TER 116 116 NA; 12431 MW;
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15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V-III REGION TUR.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Proc. Natl. Acad. Sci. U.S.A.
-!- MISCELLANEOUS: THIS CHAIN
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| 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 70.8 | 70.8 | | | 70.8 | | | | 72.9 |
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ALIGNMENTS

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Q9UL91 PRELIMINANA,
Q9UL91;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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'Serum prolactin-binding protein (PRL-BP) of human and identified as IgG.";
C. R. Acad. Sci., III, Sci. Vie 317:293-298(1994).
HSSP; P01789; IMCP.
SEQUENCE 15 AA; 1469 MW; 35ED2512FF3FA369 CRC64;
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PROLACTIN-BINDING PROTEIN (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10118;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
0.0087;
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                                                                                                          REGION (FRAGMENT).
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Q9UL88;
Q9UL88;
Q9UL88;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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Best Local Similarity 90.9
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Q9UL72;
Q9UL72;
Q9UL72;
Q9UL72;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
ENKARYOLA; Metazoa; Chordata; Cranlata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                PFAM; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                         EMBL; AF035042; AAD56278.1; HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                               INTERPRO; IPRO03006; -.
                                                                                                                                                                                                                                                                                                                                                                                         JEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                               Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. EMBL; AF035023; AAD56259.1; INTERPRO; IPR003006; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00047; 19; 1.
NON_TER 1 1
NON_TER 118 118
SEQUENCE 118 AA; 12
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MEDLINE-98277139; PubMed-9614934;
Wu X., Llu B., Van der Merwe P.L.,
Young D.C.;
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NCBL_TaxID=9606;
[1]
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Similarity 90.9%;
10; Conservative
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118 AA;
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12872 MW;
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; 12843 MW;
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90.9%;
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Pred. No. 0.094;
0; Mismatches
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0.094;
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Best Local Similarity 90.9
              Q9UL71
Q9UL71;
01-MAY-2000
01-MAY-2000
01-OCT-2000
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Q9UL90 PRELIMINARY; PRT; 113 AA.
Q9UL90; Q1-MAY-2000 (TIEMBLIE1. 13, Created)
Q1-MAY-2000 (TIEMBLIE1. 13, Last sequence update)
Q1-UN-2000 (TIEMBLIE1. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE R
EMARYOTA: Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                  INTERPRO; IPR003006; PFAM; PF00047; 19; 1.
                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035024; AAD56260.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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INTERPRO; IPR003006; -.
PFAM; PF00047; ig; 1.
NON_TER 1 1 1
NON_TER 131 131
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MEDLINE-98277139; PubMed-9614934;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                              1 EVQLVESGG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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9; Conserv
          0 (TrEMBLrel. 13, 10 (TrEMBLrel. 13, 10 (TrEMBLrel. 15, 1
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113 AA;
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Conservative 0
                                                            PRELIMINARY;
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131 AA;
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; 12437 MW;
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; 14142 MW;
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  Created)
Last sequence update)
Last annotation update)
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Pred. No.
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Last annotation update)
LIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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Pred. No.
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0.36;
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0.11;
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; Homo.
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RESULT
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Query Match Best Local S Matches 10

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Best Local S
Matches
Q9UL93;
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MEDLINE=98277139; PubMed=9614934;
Van der Merwe P.L.,
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01-MAY-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                    NON_TER
                                                                                                                                                                        PFAM;
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                                                                                                                                                                                                                     retus.";
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                                                         EVQLVESGG
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9; Conserv
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121 AA;
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122 /
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          PRELIMINARY;
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13154 MW;
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Pred. No. 0.3
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Pred. No.
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          PRT;
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                                                                                                             Length 122;
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; Homo.
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Best Local S
Matches 8
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Best Local S
Matches 8
  09UL94;
09UL94;
01-MAY-2000
01-MAY-2000
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Q9UC53;
01-MAY-2000
                                                                                                                                                                                                                                                                                                               expressed ...
syndrome cells.";
Hum. Reprod. 10:1894-1701(1995).
Hum. Reprod. 16 AA; 1626 MW; C9C5ED2512FF3FB9
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96033130; PubMed-8582963;
Shiraishi Y., Shiraishi Y., Yamamoto D., Hasegawa T., Kitamura W.,
Miki S., Tanaka T., Suzuki T., Soma H.;
"Diagnostic relevance of abortion-associated human embryonic antigen
expressed on the cell surface of tumour promoter-treated Bloom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
77 KDA SPONTANEOUS RECURRENT ABORTION-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. EMBL; AF035021; AAD56257.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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8; Conserv
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8; Conserv
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116 AA;
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  (TrEMBLrel. (TrEMBLrel.
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Primates;
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Primates;
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    13,
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Created)
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                                                                                                                                                                                                                                                                   Score 37;
Pred. No.
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Pred. No.
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Catarrhini;
                                                               PRT;
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                                                                                                                                                                                                                                             red. No. 0.62;
Mismatches
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    sequence update)
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                                                               119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
3.8;
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                                                                                                                                                                                                                                                                                      Length 16;
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AC Q5
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Q9UL92
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Best Local (
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Best Local :
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   Q9N0W4;
01-OCT-2000
                       Q9N0W4
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                NON_TER
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
Van der Merwe P.L.,
                                                                                                                                                                                             PFAM;
                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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NON_TER
SEQUENCE
                                                                                                                                                                                                     INTERPRO;
                                                                                                                                                                                                                                                    Young D.C.
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                                                                                                                     Local Similarity
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MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis
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                                                                                1 EVQLVESG 8
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                                                                    EVQLVESG
                                                                                                                                                                                      PF00047; ig; 1.
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                                                                                                                                                                                                            AF035022; AAD56258.1;
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                                                                                                                                                                                                   IPR003006;
                                                                                                                                                            124
124 AA;
 (TrEMBLrel. 15,
                                                                                                            Conservative
                     PRELIMINARY;
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                                                                                                      77.1%;
100.0%; Pr
0;
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13205 MW;
                                                                                                                                                          13580 MW;
                                                                                                        Score 37; DB; Pred. No. 6.5
Created)
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0; Mismatches
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                     PRT;
                                                                                                                                                        1BAAACBD96ACD2A2 CRC64;
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                   124
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                                                                                                                  DB 4;
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RESULT
Q9VTG0
ID Q9
AC Q9
DT 01
DT 01
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Q9UL95
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Best Local S
Matches 8
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Best Local
  Q9VTG0
Q9VTG0;
Q9VTG0;
01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Rader C., Ritter G., Nathan S., Elia M.
Rader C., Ritter G., Old L.J., Barbas C.
Cohen L.S., Well S., Old L.J., Barbas C.
"The rabbit antibody repertoire as a no
of therapeutic human antibodies.";
J. Biol. Chem. 275:13668-13676(2000).
EMBL; AF245503; AAF68450.1;
                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                      MEDLINE-98277139; PubMed-9614934; MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                        Q9UL95
Q9UL95;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2000
                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998) EMBL; AF035019; AAD56255.1; -. INTERPRO; IPR003006; -. PFAM; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                        Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence upd 01-OCT-2000 (TrEMBLrel. 15, Last annotation u ANTI-HUMAN A33 HEAVY CHARLEL (MAIN (FRAGMENT)).
                                                                  14
                                                                                               NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 QLVESGGXL
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                                                                                                                                      Similarity
8; Conserv
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8; Conser
 ) (Tremblrel. 13, of tremblrel. 13, of tremblrel. 13, of tremblrel. 14,
                                                                                                                                                                                          125
125 AA;
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124 AA;
                                                                                                                                    Conservative
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                         13516
                                                                                                                                               77.18;
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                                                                                                                                                                                         MW;
Last sequence update)
                      Created)
                                                                                                                                     0,
                                                                                                                                               Score 37;
Pred. No.
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                                           PRT;
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Pred.
                                                                                                                                                                                      0D3CD5C232488EAC CRC64;
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                       in rheumatic carditis
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                                                                                                                                                                                                                                                                                            Kalis
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No.
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CG7628 PROTEIN.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;

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RESULT 15
Q9ZXD1
ID Q9ZXD1
AC Q9ZXD1
DT 01-MAY
DT 01-MAY
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RA Addms M.D., Callker S.E., Hilt R.A., Evans C.A., Golle R.F.,
RA Admanatides P.G., Scherer S.E., Hilt R.M., Hoskins R.A., Galle R.F.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genter S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genter S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genter S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hurlis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz J., M. J., M. N.,
RA Hount S.M., Woy M., Murphy B., Murphy L., Wuzny D.M., Nelson D.L.,
RA Hount S.M., Woy M., Murphy B., Murphy L., Wuzny D.M., Nelson D.L.,
RA Holson D.R., Nelson K.A., Sannders R.D.C., Scheeler F., Shen H.,
RA Holson D.R., Weissarman D.A., Weitser D., Weissen D., Shen H.,
RA Holson D.R., Weissarman D.A., Weitser S., Wan S., San E.,
RA Holson S.M., Woodage T., Worley K.C., Wu D., Yang S., Tao Q.A.,
P. H., Shen H., Wang X., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Kang C., Stapleton M., Skupski M.P., Smith T.,
Ra Kang C., Stapleton M., Zhang G., Zhaó Q., Zheng L.,
RA Kang S., Shen H., Shang G., Zhaó Q., Zheng L.,
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Best Local S
Matches 7
Q9ZXD1 PRELIMINARY;
Q9ZXD1;
Q9ZXD1;
Q1-MAY-1999 (TrEMBLrel. 10, C.
Q1-MAY-1999 (TrEMBLrel. 10, L.
Q1-MAY-2000 (TrEMBLrel. 13, L.
DNA, COMPLETE SEQUENCE.
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2; Mismatches
                       Created)
Last sequence update)
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Matches 6; Conserv
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Inoue T., Sato T., Kobayashi Y.;

Robayashi K., Okamura K., Inoue T., Sato T., Kobayashi Y.;

Robayashi K., Okamura K., Inoue T., Sato T., Kobayashi Y.;

Robayashi K., Okamura K., Inoue T., Sato T., Kobayashi Y.;

Robayashi Y.;

Sepuence subtliss subtilis phage phi-105.";

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Inoue T., Kobayashi Y.;

Robayashi Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lambda phage group.
NCBI_TaxID=10717;
[1]
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Viruses; dsDNA viruses,
71 EIQVVEEGG 79
                                                                                         1 EVQLVESGG
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Pred. No. 12;
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Search completed: June 13, 2001, 14:29:45 Job time: 546 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/
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3: /cgn2_6/ptodata/2/
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     185757 seqs, 19210857 residues
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US-08-345-321-6
US-08-331-391A-7
US-08-331-397B-62
US-08-331-397B-62
US-08-359-31A-2
US-08-659-931A-2
US-08-467-282B-80
US-08-467-282B-80
US-08-468-739C-80
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US-08-468-739C-80
US-08-468-739C-75
US-08-75-179B-1
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Sequence 6, Appli
Sequence 7, Appli
Sequence 62, Appl
Sequence 61, Appl
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                  75, Appl
17, Appl
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| 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 |
| 95.8 | | | | 95.8 | • | | | • | | | | | | | | | |
| 116 | 116 | 116 | 116 | 116 | 116 | 115 | 115 | 115 | 114 | 114 | 114 | 114 | 114 | 113 | 111 | 109 | 109 |
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| PCT-US93-10555-10 | US-08-428-197-10 | US-08-476-349A-103 | US-08-476-349A-74 | US-08-478-039-103 | US-08-478-039-74 | US-08-767-128-36 | US-08-545-809A-122 | US-08-379-057-31 | US-09-109-207C-12 | US-09-109-207C-11 | US-08-545-809A-124 | US-08-887-352B-12 | US-08-887-352B-11 | US-08-974-899-6 | US-08-545-809A-121 | PCT-US93-10555-3 | US-08-428-197-3 |
| | Sequence 10, Appl | - | Sequence 74, Appl | • | Sequence 74, Appl | _ | • | | Sequence 12, Appl | Sequence 11, Appl | | Sequence 12, Appl | Sequence 11, Appl | Sequence 6, Appli | Sequence 121, App | Sequence 3, Appli | Sequence 3, Appli |

ALIGNMENTS

Minimum I

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TELEX: 200154

INFORMATION FOR SEQ ID NO: 10

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-809a-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-545-809A-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 102, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Funihiko
APPLICANT: MATSUDA, FUNIAN INMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE
Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/545,809A
FILING DATE: '27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                 Score 47; I
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 Mismatches
                   DB 3;
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                                   Length 119;
 Indels
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                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-345-321-6
                                                                                                                                      Sequence 7, Application US/08859931A Patent No. 5945510
                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08345321 Patent No. 5914109
                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TOPOLOGY: jin-
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 201
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,675
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 20_
TELEFAX: 248633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ZOLLA-PAZNER, SUSAN APPLICANT: GORNY, MIROSIAV K.
TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING HUMAN TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HIV-1 NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                   20 EVQLVESGGAL 30
          STREET:
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                   DDRESSEE:
                                                                                                                                                                                                                                               1 EVQLVESGGXL 11
                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     INFORMATION:
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                                                                                                       FASANO, Alessio
                                                                                                                                                                                                                                                                            Conservative
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all Seventh Street, N.W., Suite 300
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                  SUGHRUE, MION,
                                                                                                                                                                                                                                                                                      97.98;
90.98;
                                                      SUBSTANTIALLY PURE ZONULIN, A PHYSIOLOGICAL MODULATOR OF MAMMALIAN TIGHT JUNCTIONS
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ZINN, MACPEAK & SEAS
Avenue, N.W., Suite 800
                                                                                                                                                                                                                                                                                   Score 47; DB 2;
Pred. No. 0.063;
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                                                                                                                                                                                                                                                                                                Length 150;
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US-08-331-398A-62
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Best Local Sim
Matches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                      APPLICATION NUMBER: US/08/331,398J
FILLING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILLING DATE: 30-SEP-1991
                                                                                                                                    ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pastan, Ira
APPLICANT: Willingham,
APPLICANT: FitzGerald,
APPLICANT: Brinkmann, U
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: FILING DATE: 12-OC
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FILING DATE: 21 MAY 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   COUNTRY:
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MEDIUM TYPE: Floppy
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FitzGerald, Davi
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Brinkmann, Ulrich
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MBER: US 07/596,289
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ATTORNEY/AGENT INFORMATION:

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Best Local Similarity
Watches 10; Conserve
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                    TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                              ATTOMNAL, INDICATOR ANAME: HUNTER, TOM REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/767,331 FILING DATE: 30-SEP-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/596,289 FILING DATE: 12-OCT-1990 ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: peptide
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FITLE OF INVENTION:
FITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/331,3978 FILING DATE: 28-OCT-1994
                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
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                                                                     LENGTH:
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                                                    amino acid
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                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543-5043
TN NO: 62:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric and Mutationally Stabilized Tumor-
Specific Antibody Fragments, Fusion Proteins, and
                                                                                                             62:
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Pred. No. 0
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Query Match
Best Local Similarity
Watches 10; Conserv
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; MOLECULE TYPE:
US-08-759-804A-61
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                             Matches
                                         Query Match
Best Local Similarity
                                                                                                                                                                                                        TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,762
REFERNCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/596,289 FILING DATE: 12-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Relicontion Data:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Tumor-Specific Antibody Fragments.
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                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/767,331 FILING DATE: 30-SEP-1991
                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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1 EVQLVESGGXL 11
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5990296
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                                                                                                                                                            amino acid
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Willingham, P
FitzGerald, |
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                             Conservative
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                  linear
                                                                                                                 peptide
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                                         95.8%;
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                                         Score 46; DB 2
Pred. No. 0.01;
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US-08-859-931A-2
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                                                                                                                                                                     Sequence 2, Application US/08859931A Patent No. 5945510
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FASANC
                                             TITLE OF INVENTION: SUB-
TITLE OF INVENTION: PHY.
TITLE OF INVENTION: MAM-
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201 848 9228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Highet, David W
REGISTRATION NUMBER: 30,265
REFERENCE/DOCKET NUMBER: P-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 847 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 07-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
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TOPOLOGY:
                      STREET:
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                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Richard J. Rodrick, Becton, Dickinson & ADDRESSEE: Company
SEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS: 2100 Pennsylvania Avenue, N.W., Suite 800 Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid

OGY: linear
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                                                                      FASANO, Alessio
VENTION: SUBSTANTIALLY PURE ZONULIN, A
VENTION: PHYSIOLOGICAL MODULATOR OF
VENTION: MAMMALIAN TIGHT JUNCTIONS
                                                                                                                                                                                                                                                                                                                                     Conservative
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RESULT 9
US-08-471-780C-80
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                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 80, Application US/08471780C
Patent No. 5759808
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Best Local Similarity 90.1
Matches 10; Conservative
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APPLICANT: Casterman, Ceci.
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoc
NUMBER OF SEQUENCES: 130
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,780C
FILING DATE: 06-UUN-1995
           APPLICATION NUMBER: FR 9
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
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HYPOTHETICAL:
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COMPUTER READABLE FORM:
TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                     COUNTRY:
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TOPOLOGY: linear
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Jane E.R.
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                                           FR 93401310.3
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Patent No. 5800988
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Caster
APPLICANT: Hamers
                                                                    TELEPHONE: 202-408-400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                   FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Relicuration DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
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nes 10; Conservative
     TOPOLOGY: 11
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                                                    ENGTH:
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amino acid
                                  amino acid
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                                                    26 amino acids
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.55: single
linear
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Pred. No. 0.015;
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                                                                                                                                                US-08-471-282A-80
                                                 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                            TELEFAX: 202-408-4400
NFORMATION FOR SEQ ID NO:
                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Camelus dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FR 93401310.3 FILING DATE: 21-MAY 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FR 9: FILING DATE: 21-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hamers, Raymond TITLE OF INVENTION: Immuno NUMBER OF SEQUENCES: 130
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 04958.0008-00000
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                                1 EVQLVESGGXL 11
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EVQLVESGGGL 11
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90.9%;
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Pred. No. 0.015;
                                                                            Score 46; DB 2;
Pred. No. 0.015;
                                                                Mismatches
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US-08-468-739C-80
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                                                                                                                            Sequence 80, Application US/08468739C
Patent No. 6015695
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Query Match
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US-08-466-710C-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                          APPLICANT: Hamers, Raymond TITLE OF INVENTION: Immuno NUMBER OF SEQUENCES: 130 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80, Application US/08466710C Patent No. 5874541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Casterman, Cecil
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immuno;
NUMBER OF SEQUENCES: 130
                                                                                               APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Camelus dromedarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DO,
SOFTWARE: Patentin Rele.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION.
CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: US/08/106,944
FILING DATE: 17-AUG-1993
FILING DATE: FR 92402326.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005-331.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
PC-DOS/MS-DOS
PC-DOS/MS-DOS
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FR 9:
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FR 9:
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: POTTER, Jane E.R. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I S CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l: 26 amino acids amino acid
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                  Finnegan, Henderson, Farabow, Garrett & Dunner
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                                                             Immunoglobulins Devoid of Light Chains 130
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                                                                                                                                                                                                                                                                                               Score 46; DB 2; Pred. No. 0.015; 0; Mismatches
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                                                                                                                                                                                                                                                                                           0,
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US-07-977-696C-75
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Sequence 75, App
No. 5792
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US~08-468-739C-80
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Best Local Similarity
Matches 10; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                            STREET: 444 SOULD ECITY: Los Angeles
STATE: California
                                                                                                                                                               TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                  ADDRESSEE:
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APPLICATION NUMBER:
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Potter, Jane E.R. REGISTRATION NUMBER: 33. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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CLASSIFICATION: 53
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                                                                                                         E: PRETTY, SCHROEDER & POPLAWSKI
444 South Flower Street, Suite 2000
                                                                       USA
                                                                                                                                                                                                                           Peterson Dr., Jerry A. Padlan Dr., Eduardo A.
                                                                                                                                                                                                                                                      Ceriani Dr., Roberto L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 amino acids
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06-JUN-1995
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21-MAY-1993
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17-BER: FR 92402326.0
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Pred. No. 0.
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Length 26; Indels

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; MOLECULE TYPE: peptide
US-07-977-696C-75
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US-08-129-930B-75
TELE...
TELEFAX: (...
TELEX: n.a.
TELEX: n.b.
TELEX: 75
INFORMATION FOR SEQ ID NO: 75
SEQUENCE CHARACTERISTICS:
SEQUENCE: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (510) 748-6688

TELEX: n.a.

INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 75, Application US/08129930B Patent No. 5804187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.8%;
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: AMZel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
TELEPAX: (510) 748-6868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padian Dr., Edwardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
CORRESPONDENCES: 96
CORRESPONDENCE ADDRESS: ACCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NIMBER
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 11-16-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94596
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Pred. No. 0.018;
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0;

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-75

Query Match
Best Local Similarity 90.9%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 1 EVQLVESGGXL 11
Db 1 EVQLVESGGGL 11
Search completed: June 13, 2001, 14:27:07

Job time: 628 sec
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Maximum DB
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Perfect score:
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score greater than
and is derived by a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_0401:*
1: /SIDS6/gcgdata,
2: /SIDS6/gcgdata,
3: /SIDS6/gcgdata,
4: /SIDS6/gcgdata,
5: /SIDS6/gcgdata,
6: /SIDS6/gcgdata,
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100.0
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88.1
83.3
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83.3
83.3
81.0
81.0
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112:
123:
13:
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17:
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Maximum Match 100%
Listing first 45 s
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Gapop 10.0 , Gapext 0.5
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SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1987.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1987.DAT:

SIDS6/gcgdata/geneseq/geneseqp/AA1997.DAT:

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Y79137
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| 4 | σ | 4.3 | Y76636 | B58439 | Y74207 | | в28182 | W53103 | G53280 | G53281 | B14341 | Y17507 | G53282 | G21067 | Y18056 | Y18055 | G21068 | Y83931 | B52452 | в58805 | Y76536 | W52845 | R53257 | Y58575 | в07563 | B07561 | W70465 | W70463 | 7046 | 2 | 0 | ū | G52086 |
| Human cancer assoc | Amino acid sequenc | Human prostate tum | 3 | | Human prostate tum | = | Yeast transporter | Anabaena sucrose s | Arabidopsis thalia | Arabidopsis thalia | Arabidopsis thalia | S | Arabidopsis thalia | Arabidopsis thalia | 29. | | S | Mortierella alpina | Mycobacterium tube | Breast and ovarian | | A. mediterranei ri | Human collagen (Ty | um cellu | in encoded | | | Girdwood S.A.virus | South African Arbo | Chlamydia pneumoni | 7 | żs | Arabidopsis thalia |

ALIGNMENTS

RESULT Y84662

Y84662;

Y84662 standard; Protein; 8

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Human; Zot; zonula occludens toxin; zonulin; antigen presenting cell; APC; Lymphocyte proliferation; antigen; auto-immune disorder; immune related disorder; immune system rejection; multiple sclerosis; organ transplantation; inflammatory disease; allergic disease; rheumatorid arthritis; insulin dependent diabetes mellitus; celiac disease; Sjogren's syndrome; systemic lupus erythematosus; auto-immune thyroiditis; idiopathic thrombocytopenic purpura; hemolytic anemia; Grave's disease; Addison disease; autoimmune orchitis; pernicious anemia; vasculitis; autoimmune coaqulopathy; polymyositis; myasthenia gravis; polyneuritis; pemphigus; rheumatic carditis; Dermatomyositis; scleroderma; asthma; psoriasis; eczematous dermatiti 14-SEP-1998; 09-SEP-1999; 23-MAR-2000 WO200015252-A1 Synthetic Peptide antagnonist FZI/l of zonula occludens toxin (zot) polypeptide 25-JUL-2000 (first entry) Karposi's sarcoma; inflammatory bowel disease; PCR primer; ss. 98US-0100266 99WO-US18842. proliferative disorder; dermatitis;

119 4545 4550 4550

B40443 W22601

Tylactone synthase Human ORFX ORF207

G52088 G11596 G52087

W22606 G11597

Hybrid srmG/tylG o Platenolide syntha Platenolide syntha Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

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The present sequence represents a peptide antagonist of zonula occludens CC toxin (zot) polypeptide. The specification describes a method of CC suppressing antigen presenting cell (APC) mediated lymphocyte CC proliferation in a mammalian host pre-exposed to a particular antigen. CC Zot-related immunoregulator selected from Zot (zonula occludens toxin) or CC Zot-related immunoregulator selected from Zot (zonula occludens toxin) or CC The method can be used to down-regulate the activity of the APC. CC proliferation in mammalian hosts suffering from auto-immune or correct immune reputate APC-mediated lymphocyte CC immune-related disorders, immune system rejection subsequent to tissue autoimmune or immune related disorders include multiple sclerosis, correct disease, Sjogren's syndrome, systemic lupus erythematosus, auto-immune CC disease, Sjogren's syndrome, systemic lupus erythematosus, auto-immune CC disease, Sjogren's syndrome, systemic lupus erythematosus, auto-immune CC disease, Addison disease, autoimmune crititis, pernicious CC polyneuritis, autoimmune coagulopathies, myasthenia gravis, CC anemia, vasculitis, autoimmune coagulopathies, myasthenia gravis, CC Dermatomyositis, and scleroderma. The inflammatory or allergic disease, CC watposi's sarcoma, multiple sclerosis, inflammatory or allergic disease, CC conditions associated with mycotic, viral, parasitic, or bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches 8
 03-AUG-1998;
                                    28-JUL-1999;
                                                                         17-FEB-2000
                                                                                                          WO200007609-A1.
                                                                                                                                                                                       Zonulin; antagonist; zonula occludens toxin receptor; human; blood brain barrier; antiinflammatory;
                                                                                                                                                                               gastrointestinal inflammation;
                                                                                                                                                                                                                                                         Peptide FZI/1.
                                                                                                                                                                                                                                                                                    05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                               Y79137 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suppression of antigen presenting cell mediated lymphocyte proliferation, by administering a Zot-related immunoregulator useful for treating immune-related disorders, immune system rejection subsequent to tissue or organ transplantation
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98US-0127815
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The present sequence is that of peptide FZI/I, which is based on C a peptide motif (see Y79119) of human adult heart zonulin, but has a mino acid changes, corresponding to Gly at position 8, Val C at position 12 and Gln at position 13 of the adult heart zonulin CC demonstrate that there is a region spanning residues 8-15 of the C toxin (20T) that is crucial for binding to the target receptor, and CC specificity of this binding. The N-terminal sequences of human CC specificity of this binding. The N-terminal sequences of human CC identify the motif involved in receptor binding. Peptide antagonists CC (see Y79105-29) based on this motif are useful as antinflammatory CC agents for treatment of gastrointestinal inflammation, and for harriar
Sequence
                                                                                                                                                                                                                                                                                                                                                                     New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
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2199..2378
/note= "ketoreductase domain,
2469..2552
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                                                                                                       "acyltransferase domain, AT1"
                                                                                                                                                                                                                                                                            ___acyltransferase domain, AT(s)"
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                                                                                                                                                                                                                                                                                                                                                                                                     "encoded by GTG"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4155
antianaemic; gene neurodegenerative
                                             immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                      Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
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3502..3687
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3149..3477
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2576..2999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "ketoreductase
  therapy; cancer; disorder; osteoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SA,
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ntifungal; antirheumatic; antithyroid;
cancer; proliferative disorder; hyperi
osteoarthritis; graft vs host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB Pred. No. 6.6e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         ₹
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6.6e+02;
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                        hypertension
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02-MAR-1998 W22611; W22611

(first entry)

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standard;

Protein;

4545 AA

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CC C74446 to C77606 encode the proteins given in B40237 to B43397, which CC represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipociatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; CC dermatological; immunosuppressive; antiinflammatory; antidiabetic; hypotensive; CC dermatological; indunesuppressive; antithyroid; and antianaemic. The coagulant; antirheumatic; antithyroid; and antianaemic. The CC or preventing or treating pathological conditions associated with an CC or preventing or treating pathological conditions associated with an CC or proteins in gene therapy vectors. The proteins and nucleic acids may be CC used to treat cancers, proliferative disoorders, neurodegenerative CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease, CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                          Matches
                                                                                                                                                                          Query Match
Best Local
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                          Sequence
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N-PSDB; C74652.
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11111 11
31 vgvlgppg 38
                                                                   1 VGVLGRPG
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7; Conserv
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99US-0127636.
99US-0127728.
2000US-0540763.
                                                                                                                                          Conservative
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                                                                                                                                                                          83.3%;
                                                                                                                                   Score 35; DB Pred. No. 48; 0; Mismatches
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This sequence represents a hybrid protein of the invention. This sequence CC was created by replacing a EcoRI-ApaI fragment of srmg ORF1 with a CC each of the two genes is not given in the position of the residues from CC (see T80414) was isolated from Streptomyces ambofaciens, and encodes the CC multi-functional proteins which direct the synthesis of the polyketide CC platenolide. Platenolide is the basic building block of the macrolide CC synthase gene cluster of the invention. The tylG gene (see T80413) is the tylactone CC synthase gene cluster of the invention. The tylG sequence was isolated CC direct the synthesis of the polyketide CC income Streptomyces fradiae, and encodes multifunctional proteins which building block of the antiblotic tylosin. The tylG sequence can be used CC transform S. ambofaciens lacking the srmg ORF1 sequence, or S. fradiae CC lacking the tylG ORF1 sequence, so that they can produce polyketides. The CC DNA sequence can be modified so as to alter the type of carboxylic acids incorporated and/or the
                                                                                                                                                                                                                                                                                                                               Claim 23; Pages 198-212; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                            DNA encoding Streptomyces fradiae tylactone synthase domain production of tylosin-related polyketide compounds
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N-PSDB; T80415.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuhstoss
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4374..4457
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/note= "acyl carrier protein domain, ACP1, from
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/note= "ketosynthase domain, KS1, from srmg"
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WPI; 1997-418047/39
N-PSDB; T78508.
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Rosteck
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tylosin-related polyketides.
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                             SG,
                                                           LILLY
                                    Kuhstoss
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                                                        CO ELI.
                                                                                                                                                                                       /note= "dehydratase domain, 4083..4268
                                                                                                                                                                      /note= "ketoreductase domain, KR2'
4374..4457
                                                                                                                                                                                                                                3184..3520
                                                                                                                                                                                                             3546..3727
                                                                                                                                                                                                                        note-
                                                                                                                                                                                                                                                    2641..3064
                                                                                                                                                                                                                                                                                          יייטרפי "acyltransferase domain, ATI
2232..2416
                                                                                                                                                                                                                                                                                                                                                     /note= "acyltransferase domain, AT(s)" 942..1025
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                                                                                                                                                                                                                                                                                                               596..1953
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                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                    SA,
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                                                                                                                                                    "acyl carrier protein domain, ACP2"
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85.7%;
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                                                                                                                                                                                                                                                           "acyl carrier
                                                                                                                                                                                                                                                                         "ketoreductase domain, KR1"
                                                                                                                                                                                                                                                                                                                                                                          "ketosynthase domain, KS'(s)"
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Pred. No. 1.5e
1; Mismatches
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                               Richardson
                                                                                                                                                                                                                                                         protein domain,
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                                                                                                                                                                                                                                                                                                                    domain, KS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
1.5e+03;
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                                                                                                                                                                                               DH2"
                               ΜĂ
                                                                                                                                                                                                                  AT2"
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|||||
| 4223 gllgrpg 4229
                                                                                                                                                                                                                                                                            Streptomyces
                                                                                                                                                                                                                                                                                              Tylactone synthase gene cluster; tylG gene; multifunctional protein; polyketide; tylactone synthesis; antibiotic; tylosin.
                                                                                                                                                                                                                                                                                                                           Platenolide synthase
                                                                                                                                                                                                                                                                                                                                                                                      W22606 standard;
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6; Conserv
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          4083..4268
/note= "ketoreductase domain, KR2"
                                                                                                        2232..2416
/note= "ketoreductase domain, KR1"
2533..2616
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85.7%;
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                                                                             "ketosynthase domain, KS2"
                                                                                                "acyl carrier protein domain,
                                                                                                                                                                           "acyl carrier protein domain, ACP(s)"
                                                                                                                                                                                                                 "ketosynthase domain, KS'(s)"
                                                                                                                                     "acyltransferase domain, AT1"
                                                                                                                                                                                               "acyltransferase domain, AT(s)"
                                       "dehydratase
"acyl carrier protein domain, ACP2"
                                                         "acyltransferase domain, AT2"
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Pred. No. 1.5e+03;
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                                       domain,
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                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                  G11597;
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4223 gllgrpg 4229
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06-SEP-2000.
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                                                                                                                                                            termination
                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway;
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                                                                                                                                                                                  hybridisation assay;
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                                                                                                                                                                                                                                                                                                           Yeast mitochondrial COXI gene intron aIZ-encoded protein (W16303) single-stranded in a novel method for cleaving a double-stranded or single-stranded DNA substrate. The method utilises a nucleotide comprising an excised RNA transcript encoded by the group II intron group II of the COXI gene and a protein encoded by the DNA substrate in the presence of a divalent cation so that at least molecule is attached to one or both of the cleaved and a nucleic acid coxI gene in the presence of a divalent cation so that at least molecule is attached to one or both of the cleaved strands. The also be used.
                                                                                  534
                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 40-42; 58pp; English.
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N-PSDB; T63319.
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C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see Y34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffals R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
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                                                                                                                                                                                                                                                                 probable long-chai
                                                                                                                                                                                                                                                                          nypothetical prote
                                                                                                                                                                                                                                                                                     collagen COLF1 -
                                                                                                                                                                                                                                                                                                       Description
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 |
|--------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|
| 32 | 32 | 32 | 32 | 32 | 33 | 33 | 33 | <u>3</u> 3 | 33 | 33 | <u>კ</u> | 33 | ω u | 33 | <u>ω</u> |
| 76.2 | 76.2 | 76.2 | 76.2 | 76.2 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 | 78.6 |
| 203 | 184 | 178 | 178 | 161 | 26926 | . 5149 | 4735 | 4077 | 2944 | 2569 | 2514 | 2512 | 2297 | 2129 | 1843 |
| 2 | N | N | _ | N | _ | N | N | N | N | N | ۲ | _ | N | N | N |
| A72705 | S60245 | S45049 | R5RT11 | F72593 | I38344 | F83345 | T17463 | T17484 | A54849 | T14164 | MNWV82 | SAMIN | T34918 | T14182 | S18803 |
| | ribosomal protein | ribosomal protein | ribosomal protein | hypothetical prote | titin, cardiac mus | probable non-ribos | rifamycin polyket: | hypothetical prote | collagen alpha 1(| peptide synthetas | nonstructural poly | nonstructural poly | polyketide synthas | fxbC protein - My | collagen alpha 1(|

ALIGNMENTS

C;Species: Ephydatia muelleri
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C;Accession: S31521
R;Exposito, J:Y: van der Rest, M.; Garrone, R.
submitted to the EMBL Data Library, December 1992
A;Description: The complete intron/exon structure of E. muelleri collagen gan A;Reference number: S31521
A;Accession: S31521

muelleri collagen gene sugges

collagen COLF1 -

freshwater sponge (Ephydatia muelleri)

A;Cross-references: EMBL:x69818; NID:g429036; PIDN:CAA49472.1; PID:g9300 C;Superfamily: unassigned collagens

2:

Length 812;

A; Molecule type: mRNA A; Residues: 1-812 <EXP>

A; Status: preliminary

```
C;Accession: G83359
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: G83359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
"-+ches 7; Conservations
                                                                                                                          A; Experimental source: strain PAO1 C; Genetics:
                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-485 <STO>
A;Cross-references: GB:AE004654; GB:AE004091; NID:g9948311; PIDN:AAG05671.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein PA2283 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                           A; Gene: PA2283
                     Query Match
Best Local
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                     85.7%;
75.0%;
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Score 36; DB Pred. No. 36; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 25;
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                                           2
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                                           Length 485,
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Local Similarity hes 6; Conserv

Conservative

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Gaps

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                                                                                                                                    A:Cross-references: GDB:582527
A:Map position: Xp22.3-Xp22.3
C:Superfamily: GLGF domain homology
F:32-104/Domain: GLGF domain homology <GLG>
                                                                                                                                                                                                                        A;Cross-references: EMBL:x83543; NID:g790999; PIDN:CAA58534.1;
                                                                                                                                                                                                                                                                              Hum. Mol. Genet. 4, 373-382, 1995
A:TitLe: Cloning of a human homologue of the Xenopus laevis APX gene from the ocular all
A:Reference number: 137183; MUID:95315933
                                                                                                                                                                                                            A; Gene: GDB:APXL
                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-1616 < RES>
                                                                                                                                                                                                                                                                                                                                                                       gene APXL protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: 137183
                                                                                                                                                                                                                                                                                                                                 R;Schiaffino, M.V.; Bassi, M.T.; Rugarli, E.I.; Renieri, A.; Galli, L.; Ballabio,
Hum. Mol. Genet. 4, 373-382, 1995
                                                                                  Query Match
Best Local
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C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA
C:Keywords: acid-thiol ligase; coenzyme A
F;85-561/Domain: acetate--CoA ligase homology <ACL>
                                                                        Matches
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A;Residues: 1-577 <MHI>
A;Croos-references: GB:AEE001863; GB:AEE001825; NID:96460670;
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: DRA0309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K; White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; M.; Shen, M.; Vanmathevan, J.J.; Lam, P.; McDonald, L.; U.S.; Snith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium D. A; Reference number a75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) DRA0309 [similarity]
C:Species: Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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1087 VGVLGRP 1093
                                                                   Local Similarity
les 7; Conserv
                                  1 VGVLGRP 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
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                                                               Conservative
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                                                            0;
                                                                           Score 36;
Pred. No.
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42;
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; Utterback,
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                                                                                                                                                                                                                       PID:g1181628
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T.; Zalewski,
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Collagen alpha 1(IV) chain - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1992 #sequence_revision 05-Apr-1995
C;Accession: A39474; S16907; S18422; A39419
C;Accession: A39474; S16907; S18422; A39419
J. Biol. Chem. 266, 14088-14094, 1991
A;Title: Properties of the collagenous domain of the helical structure and noncollagenous domain.
                                                                                                                                                                            RESULT
S16907
                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Rv3218
C;Superfamily: Mycobacterium tuberculosis hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Z95120;
A;Experimental source: strain H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-321 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A;Title: Deciphering the biology of Mycobacterium
A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C70596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Rv3218 – Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
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Best Local
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A:Molecule type: DNA
A:Residues: 1-317 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable integral membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Decies: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 R;Seeger, S; Harris, D; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandre to the EMBL Data Library, June 1999
A;Reference number: Z21565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
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Best Local Similarity 75.
Matches 6; Conservative
                                                                                                                                                                                                                                               73 GMLGRPG 79
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nes 6; Conserv
                                                                                                                                                                                                                                                                                    2 GVLGRPG 8
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75.0%;
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Pred. No. 37;
1; Mismatches
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              the alpha3(IV) chain, the
                                                                                                                                                                                                                                                                                                                                             2
                                                                                             #text_change
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                                                                                         19-Oct-1995
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          Goodpastur
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Holroyd,
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RESULT
CGHU1B
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A; Molecule type: protein
A; Residues: 337-347, Ft.', 350-356 <GU3>
A; Residues: 337-347, Ft.', 350-356 <GU3>
C; Superfamily: collagen alpha 1(IV) chain
C; Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
C; Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F; 31, 34, 37, 46, 61, 69, 78, 84, 87, 102, 110, 122, 125, 137, 140, 143, 149, 155, 158, 161, 164, 185, 188, 199
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A;Moslecule type: protein
A;Residues: 337-347, 'FL', '50-353 <BU2>
R;Gunwar, S.; Ballester, F.; Kalluri, R.; Timoneda, J.; Chonko, A.M.; Edwards,
J. Biol. Chem. 266, 15318-15324, 1991
A;Title: Glomerular basement membrane. Identification of dimeric subunits of th
A;Reference number: A39419; MUID:91332055
A;Accession: A39419
                                                                                                                                                                                                                                   A;Residues: 1-411 <COL>
A;Cross-references: GB:Z83859; GB:AL123456; NID:g3261678;
A;Experimental source: strain H37Rv
                                                                                    S
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C; Superfamily:
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A; Residues: 1-411 <C
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Best Local (
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                                                          311 GMLGRPG
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                                                                                                                  Local Similarity
nes 6; Conserv
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                                                                                                                                83.3%;
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62.5%;
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                                                                                                                                                                                                                                                   PIDN:CAB06118.1;
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                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          Gordon,
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F:62-1466/Region: Interrupted helical
F:94-96/Region: cell attachment (R-G-D) motif
F:94-96/Region: cell attachment (R-G-D) motif
F:145-147/Region: cell attachment (R-G-D) motif
F:189-191/Region: cell attachment (R-G-D) motif
F:189-191/Region: cell attachment (R-G-D) motif
F:724-726/Region: cell attachment (R-G-D) motif
F:724-726/Region: cell attachment (R-G-D) motif
F:785-787/Region: cell attachment (R-G-D) motif
F:1989-991/Region: cell attachment (R-G-D) motif
F:1212-1214/Region: cell attachment (R-G-D) motif
F:1471-1569/Domain: collagen IV carboxyl-terminal repeat <CT1>F:1471-1569/Domain: collagen IV carboxyl-terminal repeat <CT2>F:1471-1569/Domain: collagen IV carboxyl-terminal repeat <CT2>F:147,52,55,57,266,400,460,492,494,668,790,828,1095,1131,1294,1317,1375,1407/Disulfide
F:1480-1566,1513-1569/Disulfide bonds: (or 1480-1569) 1513-1566) #status predicted
F:1525-1531,1634-1641/Disulfide bonds: #status predicted
F:1588-1683,1622-1686/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:132673; OMIM:120131
A;Map position: 2q35-2q37
A;Introns: 39/1; 1406/1; 1445/1; 1508/1; 1603/3 *status incomplete
A;Note: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strands w C;Complex: this minor type IV collagen is thought to form a heterotrimer of two alpha mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimerier associations in the interrupted helical domain (with disulfide and desmosine cross C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: minor structural component of extracellular basement membrane in C; Superfamily: collagen alpha 1(IV) chain C; Keywords: basement membrane; coiled coil; extracellular matrix; glycoprotein; F;1-38/Domain: signal sequence #status predicted <SIC> F;39-1690/Product: collagen alpha 4(IV) chain #status predicted <MAT> F;39-61/Domain: mino-terminal nonhelical, NH1 <NH1>
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A; Residues: 1-1690 < LEI>
A; Residues: 1-1690 < LEI>
A; Cross - references: GB:X81053; NID:g574805; PIDN:CAA56943.1; PID:g574806
R:Sugimoto, M.; Oohashi, T.; Yoshioka, H.; Matsuo, N.; Ninomiya, Y.
FEBS Lett. 330, 122-128, 1993
R:FEBS Lett. 330, 122-128, 1993
A; Title: CDNA isolation and partial gene structure of the human alpha-4(A; Reference number: S36854; MUID:93374047
A; Accession: S36854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1407-1424 'G',1426-1430,'A',1432-1439,'L',1441-1507 A; Cross-references: GB:L01475; GB:L01476 A; Note: the codons given for 1438-Asp (GAG) and 1443-Gly (GCA) a C; Comment: Prolines and lysines at the third position of the tried and subsequently 0-glycosylated.
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A;Residues: 1219-1658, FE',1661-1690 <SUG>
A;Cross-references: DDBJ:D17391; NID:g440365;
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A;Accession: A55360
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Query Match

Best Local Similarity
Matches 6; Conserv

83.3%;

Score 35; DB 1; Pred. No. 1.8e+02; 1; Mismatches 0

Length 1690

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hypothetical protein F32G8.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
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A:Introns: 87/1
C:Superfamily: unassigned collagens
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C;Species: Caenorhabditis elegans
C;Dete: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Accession: T32921
R;Madsen, C.; Graves, T.; Blair, T.
submitted to the EMBL Data Library, January 1998
A;Bescription: The sequence of C. elegans cosmid K09H9.
A;Reference number: Z21247
A;Accession: T32921
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AF043700; PIDN:AAB97570.1; GSPDB:GN00019; CESP:K09H9.3
A;Experimental source: strain Bristol N2; clone K09H9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-283 <MAD>
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Best Local Similarity 75.0
6; Conservative
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A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Mossiduse: 1-3198 <EXPS
A;Cross-references: GB:M92041; NID:g161448; PIDN:AAA30040.1; PID:g161449
A;Cross-reference extracted from NCBI backbone (NCBIP:111965)
C;Superfamily: unassigned collagens; fibrillar collagen carboxyl-terminal homology; von F;48-106/Domain: von Willebrand factor type C repeat homology <VWC>
F;3978-3198/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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A:Accession: A43426
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R; Exposito, J.Y.
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Best Local Similarity
Matches 6; Conserv
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267, 17404-17408, 1992
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75.0%;
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Pred. No. 50;
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Pred. No.
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hes 1; Indels
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A; Molecule type: DNA
A; Residues: 1-324 <KRA>
A; Cross -references: GB:JI
C; Genetics:
A; Introns: 47/3
C; Superfamily: unassigne
                                                                                       R;Kramer, J.M.; Johnson, J.J.; Edgar, R.S.; Basch, C.; Roberts, S. Cell 55, 555-565, 1988
A;Title: The sqt-1 gene of C. elegans encodes a collagen critical A;Reference number: A31920; MUID:89028667
A;Accession: A31920
                                                                                                                                                                           collagen sqt-1 precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Sep-1999
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A; Residues: 1-324 <WIL>
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A;Reference number: Z19019
A;Accession: T18763
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A:Introns: 47/3
C:Superfamily: unassigned collagens
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A; Residues: 1-294 <WIL>
A; Cross references: EMBL: 272509; pIDN: CAA96649.1; GSPDB: GN00023; CESP: F32G8.5
A; Experimental source: clone F32G8
C; Genetics:
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submitted to the EMBL Data Library,
"""raference number: Z19456
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Best Local :
                                                                                                                                                                                                                                                                                                              178 GALGRPG 184
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                                          GB:J03146; NID:g156445;
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unassigned collagens

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collagen alpha 3(V) chain - human (fragments)
c;Species: Homo sapiens (man)
c;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-May-1997
c;Accession: S20375
R;Mann, K.
Blol. Chem. Hoppe-Seyler 373, 69-75, 1992
A:Title: Isolation of the alpha-3-chain of human type V collagen and characterization by A;Reference number: S20375; MUID:92239022
A;Accession: S20375
A;Status: proliminary
A;Status: proliminary
A;Residues: 1-382 <MAN>
c;Superfamily: unassigned collagens
Search completed: June 13, 2001, 14:23:12 Job time: 743 sec
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S20375
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    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
   93435 segs, 34255486 residues
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BISC_RHOSH
CAII_HUMAN
RLI1_PIG
RLI1_HUMAN
RLI1_DROME
RIBB_BUCAI
NODG_RHIS3
PGK_ZYMMO
COLQ_HUMAN
YH92_CABELL
NUSC_SYNY3
SKNL_YEAST
YKNP_YEAST
YN99_YEAST
YN99_YEAST
YN99_YEAST
YN91_CANALL
CDR1_CANALL
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 CDR3_CANAL
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Q9y215
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1 corynebacte
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6 saccharomyc
7 canis famil
7 candida alb
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8 candida alb
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2 drosophila
7 buchnera ap
2 rhizobium s
4 zymomonas m
5 homo sapien
6 caenorhabdi
9 synechocyst
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | |
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| COLO_MOUSE | BEXA_HAEIN | CTRD_NEIMB | CTRD_NEIMA | Y814_ARCFU | PLE1_RAT | CA1B_HUMAN | CA14_DROME | PDRA_YEAST | PDRF_YEAST | PDR5_YEAST | SNQ2_YEAST | |
| O35348 mus musculu | _ | | | 029444 archaeoglob | | P12107 homo sapien | P08120 drosophila | | Q04182 saccharomyc | P33302 saccharomyc | P32568 saccharomyc | |

ALIGNMENTS

| S T T T T T T T T T T T T T T T T T T T | 88888888 | CCCCRRRR | R R R R R R R R R R R R R R R R R R R | 88888 | RESULT APXL_H ID A AC Q DT 0 DT 0 DT 0 DT 0 DT 0 |
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| EMBL; X83543; EMBL; AC002365 HSSP; Q12959; MIM; 300103; - InterPro; IPRO InterPro; IPRO Pfam; PF00219; Pfam; PF00219; Pfam; PF09595; PROSITE; PS501 SIMILAR 15 DOMAIN 15 DOMAIN 31 DOMAIN 34 DOMAIN 106 SEQUENCE 161 | This SWISS- between th the European use by no modified an entitles re- or send an | [2] [2] [2] [2] [2] [3] [4] [5] [5] [5] [6] [7] [7] [7] [7] [7] [7] [8] [7] [8] [7] [8] [7] [8] [8] [8] [8] [8] [8] [8] [8] [8] [8 | (1) SEQUENCE FROM TISSUE-Retina; TISSUE-Retina; MEDLINE-953159 Schlaffino V.M Ballabio A.; "Cloning of a ocular albinis Hum. Mol Gene | APXL. Homo sapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606; | RESULT 1 APXL_HUMAN ID APXL_HUMAN AC Q13796; DT 01-NOV-1997 DT 01-CVT-2000 DE APICAL-LIKE |
| TO MOUSE SYNTROPHIN-1 AND RABBIT DYSTROPHIN-ASSOCIATED PROTEIN. POLY-SER. POLY-PRO. POLY-PRO. POLY-PRO. POLY-PRO. 752406B5BC0B60A2 CRC64; | T entry is copyright. It is produced through a c wiss Institute of Bioinformatics and the EMBL ichiformatics Institute. There are no restrict rofit institutions as long as its content is his statement is not removed. Usage by and fores a license agreement (See http://www.isb-sib.tl. to license@isb-sib.ch). | ENCE OF 56-1616 FROM N.A. Y., Gibbs R.A.; Itted (JAN-1997) to the EMBL/GenBank/DDBJ databases. TISSUE SPECIFICITY: ABUNDANT IN RETINA AND MELANOMA; ALSO IN BRAIN, PLACENTA, LUNG, KIDNEY, PANCREAS. SIMILARITY: SOME, TO XENOPUS LAEVIS APICAL PROTEIN (APX). | [1] SEQUENCE FROM N.A. TISSUE=Retina; MISDLINE=9531593; PubMed=7795590; Schlaffino V.M., Bassi M.T., Rugarli E.I., Renieri A., Galli L., Ballabio A.; "Cloning of a human homologue of the Xenopus laevis APX gene from the "Coular albinism type i critical region."; Hum. Mol. Genet. 4:373-382(1995). | ns (Human). Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.)=9606; | STANDARD; PRT; 1616 AA. 7 (Rel. 35, Created) 7 (Rel. 35, Last sequence update) 0 (Rel. 40, Last annotation update) E PROTEIN (APXL PROTEIN). |

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Matches
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J. Clin.
                                                                                                                                        VARIANT AS SER-1201.

WEDLING-95078927; PubMed-7987396;

MCDLING-95078927; PubMed-7987396;

Mochizuki T., Lemmink H.H., Mariyama M., Antignac C., Gubler M., Pirson Y., Verellen-Dumoulin C., Chan B., Schroeder C.H., Smeets H.J., Reeders S.T.;

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Nat. Genet. 8:77-82(1994).
VARIANTS AS, AND VARIANTS MEDLINE-99011253; PubMed-
                                                  Lemmink H.H., Nillesen W.N., Mc
Brunner H.G., van Oost B.A., Mc
"Benign familial hematuria due
alpha4 gene.";
                                                                                                      VARIANT BEH GLU-897.
MEDLINE-96379660; PubMed-8787673;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1407-1507 FROM N.A.

MEDLINE-93054733; PubMed-1429714;

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"Isolation and sequencing of cDNAs and genomic DNAs encoding the alpha 4 chain of basement membrane collagen type IV and assignment the gene to the distal long arm of human chromosome 2.";

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                                                                                                                                                                                                                                                               Lemmink H.H., Schroeder C.H., Monnens L.A.H., Smeets H.J.M.; "The clinical spectrum of type IV collagen mutations."; Hum. Mutat. 9:477-499(1997).
                                                                                                                                                                                                                                                                                                            MEDLINE-97338662; PubMed-9195222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93374047; PubMed-8365481;
Sugimoto M., Oohashi T., Yoshioka H., Matsuo N., Ninomiya Y.;
"CDNA isolation and partial gene structure of the human alpha collagen chain.";
                                                                                                                                                                                                                                                                                                                                 REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEBS Lett. 330:122-128(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).

Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leinonen A., Mariyama M., Mochizuki T., Tryggvason K., Reeders S.T.; "Complete primary structure of the human type IV collagen alpha 4(TV) chain. Comparison with structure and expression of the other alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95014445; PubMed=7523402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                        Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 1219-1690 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chem. 269:26172-26177(1994).
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7; Conser
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                                                                            Mochizuki T.,
Monnens L.A.H.
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Pred. No.
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                                                               mutation
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67;
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                                                                           Schroeder C.
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                                                           type IV collagen
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IV COLLAGENS.

-!- DISEASE: DEFECTS IN COL4A4 ARE ASSOCIATED WITH THE TYPE II AUTOSOMAL RECESSIVE FORM OF ALPORT SYNDROME (AS), AN HEREDITARY GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE RENAL FAILURE, HEMATURIA AND DEAFNESS. THE RECESSIVE FORM OCCURS EQUALLY BETWEEN HEMATURIA AND DEAFNESS. THE RECESSIVE FORM OCCURS EQUALLY BETWEEN MALES AND FEMALES.

-!- DISEASE: DEFECTS IN COL4A4 ARE ASSOCIATED WITH FAMILIAL BENIGN CHARACTERIZED BY PERSISTENT HEMATURIA, AN ELECTRON MICROSCOPICALLY DETECTABLE THIN GLOMERULAR BASEMENT MEMBRANE GIBBLAND AND AN AUTOSSOMAL DOMINANT MODE OF INHERITANCE RENAL FUNCTION REMAINS NORMAL. IN CHILDREN DIFFERENTIATION BETWEEN FBH AND AS CAN BE DIFFICULT, BECAUSE BOTH DISORDERS ARE MANIFESTED BY PERSISTENT HEMATURIA, AND THIN GBM AT THAT AGE.

-!- SIMILARITY: TO OTHER TYPE IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA 6(IV). ACH OF MICH CAN FORM A TRIPLE HELIX STRUCTURE WITH 2 OPHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

-!- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).
-!- TISSUE SPECIFICITY: ALPHA 3 AND ALPHA 4 TYPE IV COLLAGENS ARE COCCLEA, LUNG AND BRAIN.
-!- TOUGHT CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS OF KIDNEY, EYE, COCLLEA, LUNG AND BRAIN.
-!- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.
-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPLE THEIR CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.
-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPLE THAINS.
-!- PTM: TYPE IV COLLAGENS CONTAIN NUMBEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF THE CALAGENS.
--- ARE INVOLVED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boye E., Mollet G., Forestier L., Cohen-Solal L., Heidet L., Cochat P., Gruenfeld J.-P., Palcoux J.-B., Gubler M.-C., Antignac "Determination of the genomic structure of the COL4A4 gene and of novel mutations causing autosomal recessive Alport syndrome.",

Am. J. Hum. Genet. 63:1329-1340(1998).

-I- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE' MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
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                                                                                                      InterPro; IPR000087; -.
InterPro; IPR001442; -.
Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen; 20.
Extracellular matrix; Connective tissue; Basement membrane; Repeat; Extracellular matrix; Glycoprotein; Signal; Disease mutation;
                                                                                           CHAIN
                                                                                                                                                                                                   EMBL;
                                                                                                                                                                               MIM; 203780;
                                                                                                                                                                                                  ; X81053; CAA56943.1; -.; D17391; BAA04214.1; -. 120131; -.
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TRIPLE-HELICAL
                                               NONHELICAL REGION CELL ATTACHMENT SI
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COLLAGEN ALPHA
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E (POTENTIAL).
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Query Match
Best Local Similarity
Matches 6; Conser
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DISULFID
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DISULFID
                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2:
MEDLINE-89028667; PubMed-3180220;
MEDLINE-89028667; PubMed-3180220;
MEDLINE-89028667; PubMed-3180220;
The sqt-1 gene of C. elegans encodes a rankamal morphogeneals.";
Cell 55:555-565(1988).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
                                                                                                                                                     SQT-1 OR ROL-5 OR B0491.2.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                          01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CUTICLE COLLAGEN SQT-1.
                                                                                                                                                                                                                     P12114; Q17509;
01-OCT-1989 (Rel.
                                                                                                                                                                                                                                                   CAEEL
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                              Sulston J.
                                      STRAIN-BRISTOL N2;
                                                 SEQUENCE
                                                                                                                                           NCBI_TaxID-6239;
                                                                                                                                                                                                                                        CCS1_CAEEL
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1 AA;
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rinae; Caenorhabditis.
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OR 1569 (BY SIMILARITY).
BY SIMILARITY.
OR 1683 (BY SIMILARITY).
OR 1686 (BY SIMILARITY).
BY SIMILARITY.
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G -> V (IN AS).

/FTId=VAR_008153.

G -> S (IN AS).

/FTId=VAR_001913.
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G -> A
                                                                                                                                                                                                                                                                                                                                     Score 35; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL ATTACHMENT SITE (POTENTIAL).
CLEAVAGE (BY COLLAGENASE)
(BY SIMILARITY).
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_008154.

p -> L (IN AS).
/FTId=VAR_008155.

LQ -> FE (IN REF. 2).
LQ -> FE (IN REF. 2).
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N-LINKED (GLCNAC. .
MISSING (IN AS).
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/FTId=VAR_001912.
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                                                                                    a collagen critical for
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RESULT 4
CA35_HUMAN
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Best Local S
Matches 6
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01-MAY-1992
01-MAY-1992
01-OCT-2000
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                            COLLAGEN ALPHA COL5A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J03146; AAA65468.1; -. EMBL; Z49907; CAA90084.1; -. PIR; A31920; A31920. WormPep; B0491.2; CE02104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>:</del>
                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                          TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                    CA35_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cuticle;
                                                                                                                                                   Mann K.;
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                 Homo sapiens (Human).
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                                                                                                                                                             MEDLINE=92239022;
                                                                                                                                                                                                                                                                                                                                                                                               178 GALGRPG
                                                                                                                                                                                                                                                                                                                                                                                                            2 GVLGRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKS.
DISEASE: THIS IS A COLLAGEN CRITICAL FOR ORGANISMAL DISEASE: THIS OF A COLLAGEN CRITICAL FOR ORGANISMAL OF THE SOT-1 CAN LENGTHEN, SHORTEN, OR HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTATIONS IN SQT-1 CAN LENGTHEN,
ENTIRE ANIMAL.
SIMILARITY: TO OTHER COLLAGENS. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BARRIER TO PROTECT THE WORM FROM ITS SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS CUTICLE BY DISULFIDE BONDS AND OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLAGENS. ROL-6 AND SQT-1 BELONGS AND MAY ALSO PHYSICALLY INTERACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Connective 1 127 1: 171 2: 237 2: 158 1: 158 1: 238 2: E 324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000087;
                                                                                                                                                                                                                                                                                 (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                               184
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                                                                                                                                                                                                                                                                                                                                    STANDARD;
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153
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Primates;
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85.7%;
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                                                                                                                                                                                                                                                                       (FRAGMENTS).
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TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
V >> A (IN REF. 2).
V -> A (IN REF. 2).
MW; DBAC00826993C1CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred.
                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                    382 AA
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ARE COMPLEXED WITHIN THE
TYPES OF COVALENT CROSS-
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Pfam; PF01391; Collagen; 2.
Hypothetical protein; Cuticle; Connective Multigene family; Collagen.
DOMAIN
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DOMAIN
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Best Local
                                                                                                       EMBL; U80441; AAB37656.1; -. WormPep; F27C1.8; CE09720.
                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                            STRAIN-BISTOL W:

WU X., Le T.T.;

WU X., Le T.T.;

SUBMITTED (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGEILY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).

CUTICLE BY DISULTIDE BONDS AND OTHER TYPES OF COVALENT CROSS-LINKS (BY SIMILARITY).

COLLAGEN COLLAGENS. STRONG, TO OTHER CUTICLE

COLLAGENS.
                                                                                     InterPro; IPR000087; InterPro; IPR002486; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          YKNP_CAEEL STANDARD; P91285; Created)
01-WOV-1997 (Rel. 35, Cast seq
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
Eukaryota; Metazoa; Ner
Rhabditidae; Peloderin
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence up
PUTATIVE CUTICLE COLLAGEN F27C1.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAEEL
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NON_TER
SEQUENCE
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; S20375; S20375.
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6; Conserv
         284 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Peloderinae;
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317
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        28216 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.0%;
75.0%;
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           TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
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8EED98AED554B454 CRC64;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                         tissue; Repeat;
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δõ

1 VGVLGRPG

Matches

Similarity

Conservative

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1;

Length 353;

0,

Gaps

0,

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Query Match
Best Local
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A Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
A Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
A Motomura K., Nakade S., Nakamura Y., Nahimoto H., Nishio Y.,
A Motomura K., Nakade S., Nakamura Y., Nahimoto H., Nishio Y.,
Takada J., Takemoto K., Sivasundaram. S.,
A Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
A Yamamoto Y., Horiuchi T.;
Takada J., Takemoto K., Takeuchi Y., Wada C.,
Takeuchi T.,
A 570-kb DNA sequence of the Escherichia coli K-12 genome Corresponding to the 28.0-40.1 min region on the linkage map.",
Corresponding to the 28.0-40.1 min region on the linkage map.",
Corresponding to the Stones To THE L4BD FAMILY OF NADP-DEPENDENT
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                                                                                                   EMBL; AE000242; AAC74531.1; ALT_INIT.
EMBL; D90784; BAA15081.1; -
EMBL; D90785; BAA15084.1; -
EcoGene; EG13772; YncB.
                                                                                 SEQUENCE
                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                            Hypothetical protein;
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrictions of the European Bioinformatics institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bu Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhe Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose "The Complete genome sequence of Escherichia coli K-12.";
science 277:1453-1474(1997).
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P76113; P78255;
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Bacteria; Proteobacteria;
Escherichia.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE NADP-DEPENDENT OXIDOREDUCTASE IN TEHB-RHSE INTERGENIC
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K., Mayhew G.F.,
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RESULT 7
COLQ_TORMA
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Ol-JUN-1994 (Rel. 29, Last sequence update)
Ol-OCT-1994 (Rel. 30, Last annotation update)
ACETYLCHOLINESTERASE COLLAGENIC TAIL PEPTIDE SUBUNIT).
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Q03637;
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                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement by Institute is a bioinformatic and the Extra the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       Deprez P., Inestrosa N.C.;
"Molecular modeling of the collagen-like tail of acetylcholinesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duval N., Krejci E., Grassi J., Coussen F., Massoulie J., Bon S. "Molecular architecture of acetylcholinesterase collagen-tailed forms; construction of a glycollpid-tailed tetramer."; EMBO J. 11:3255-3261(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Torpedo marmorata (Marbled electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Cheukaryota; Metazoa; Chordata; Craniata; Pristiorajea; Elasmobranchil; Squalea; Hypnosqualea; Pristiorajea; Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                                                         Protein Eng. 13:27-34(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20146083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Quaternary associations of acetylcholinesterase. attachment domain of the collagen tail."; J. Biol. Chem. 272:3016-3021(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION OF PRO-RICH ATTACHMENT MEDLINE-97160616; Pubmed-9006950;
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NCBI_TaxID=7788;
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MEDLINE-91216124; PubMed-1840520;
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                                                                                                                                                                      MUSCLE.

DOMAIN: THE PROLINE-RICH AT CATALYTIC SUBUNITS.

SIMILARITY: BELONGS TO THE
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SYNAPTIC BASAL LAMINA.

SUBUNIT: THE ASYMMETRIC FORM OF ACHE IS A DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (0) AND A VARIABLE NUMBER OF ASYMMETRIC (T) CATALYTIC SUBUNITS. THE N-TERMINAL OF COLLAGENIC SUBUNIT (Q) ASSOCIATES WITH THE C-TERMINAL OF THE CATALYTIC SUBUNIT (T).

TISSUE SPECIFICITY: EXPRESSED IN ELECTRIC ORGANS BUT NOT IN
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x59359; CAA42009.1;
S15035; S15035.
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See a license agreement (See
                                                                                                                                                                                    "Molecular cloning and expression of biotin sulfoxide reductase fr
Rhodobacter sphaeroides forma sp. denitrificans.";
Arch. Biochem. Biophys. 318:322-332(1995).
-i- FUNCTION: THIS ENZYME MAY SERVE AS A SCAVENGER, ALLOWING THE C
TO UTILIZE BIOTIN SULFOXIDE AS A BIOTIN SOURCE (BY SIMILARITY)
-i- CATALYTIC ACTIVITY: REDUCES A SPONTANEOUS OXIDATION PRODUCT OF
BIOTIN, D-BIOTIN D-SULFOXIDE (BSO OR BDS), BACK TO BIOTIN.
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REPEAT
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                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                    -!- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
-!- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING OXIDOREDUCTASE FAMILY.
                                                                                                                                                                                                                                                                 STRAIN=F. SP. DENITRIFICANS IL106; MEDLINE=95251380; PubMed=7733660; Pollock V.V., Barber M.J.;
                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
BIOTIN SULFOXIDE REDUCTASE (EC 1.-.-.
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or send an email t
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Bacteria; Proteobacteria;
InterPro; IPR001467;
Pfam; PF01568; Molydc
Pfam; PF00384; molybd
                                EMBL; U08189; AAA74739.1; HSSP; Q57366; 1CXT.
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COLLAGEN-LIKE.
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PEPTIDE.
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molydop_binding; molybdopterin; 1

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Query Best L

Matches

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PARTIAL SEQUENCE FROM N.A.
MEDLINE-86196099; Pubmed-3009468;
Sakurai Y., Sullivan M., Yamada Y.;
"Alpha 1 type IV collagen gene evol
                                                                                                                                                                                     SEQUENCE OF 1441-1669 FROM N.A.-
MEDLINE-87250460; PubMed-3597383;
Kurkinen M., Condon M.R., Blumber
Saus J., Pihlajaniemi T.;
                                                                                                                                                                                                                                                                                                            Oberbaeumer I., Laurent M., Schwarz U., Sakurai Y., Yamada Y., Vogell G., Vogs T., Siebold B., Glanville R.W., Kuhn K., "Amino acid sequence of the non-collagenous globular domain (NCI) of the alpha 1(IV) chain of basement membrane collagen as derived from complementary DNA.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLAA1.
COLAA1.
Mus musculus (Mouse).
Mus musculus (Mouse).
Theria; Rodentia; C;
                                                                                                            "Extensive homology between the carboxyl-terminal peptides lipha 1(IV) and alpha 2(IV) collagen."; []. Biol. Chem. 262:8496-8499(1987).
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1276-1669 FROM N.A. MEDLINE-85127033; PubMed-2578961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nath P., Laurent M., Horn E., Sobel M.E., "Isolation of an alpha 1 type-IV collagen synthetic oligodeoxynucleotide.", Gene 43:301-304(1986).
                                                                                                                                                                                                                                                                                                                                                                                             Oberbaeumer
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MEDLINE-88112221; PubMed-3338568;

Wood L., Theriault N., Vogeli G.;

"CDNA clones completing the nucleotide and derived sequence of the alpha I chain of basement membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-86301886;
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Muthkumaran G., Blumberg B., Kurkinen M.;
"The complete primary structure for the alpha 1-chain
collagen IV. Differential evolution of collagen IV don
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01-FEB-1991 (Rel. 17, Last sequence update)
15-7UL-1999 (Rel. 38, Last annotation update)
COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
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PROSITE; PS00490; M
PROSITE; PS00932; M
Ox1doreductase; MO1
SEQUENCE 744 AA;
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P02463;
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Lett. 227:5-8(1988).
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01886; PubMed=3755692;
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J. Biol.
                                                                                                                                                                                                                                                                                                        L; J03758; AAA37439.1; — M3333; AAA51625.1; — M3333; AAA51625.1; — M36777; CAA29946.1; — M20201; CAA26132.1; — M18582; AAA37340.1; — M13072; AAA37343.1; — M13072; AAA3734372; AAA3734372; AAA3734372; AAA3734372; AAA3734372; AAA3734372; AAA3734
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R EMBL; M14042; AAA77342.1;

R EMBL, M12879; AAA77343.1;

R EMBL, M13024; -; NOT_ANNOTATED_CDS.

R EMBL, M13025; -; NOT_ANNOTATED_CDS.

R EMBL, M13026; AAA37344.1;

R EMBL; M13026; AAA37346.1; -;

R EMBL; M13027; AAA37346.1; -;

R EMBL; M13043; AAA37346.1; -;

R EMBL; J04448; AAA37437.1; -;

R EMBL; J04448; AAA37446.1; -;

R EMBL; J04448; AAA37437.1; -;

R EMBL; J04448; AAA37446.1; -;

R EMBL; J04448; AAA37446.1; -;

R EMBL; J04448; AAA3746.1; -;

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SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK,
DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
G-X'Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 75 DOMAIN.

"I PTM: PROLINGS AT THE THIRD POSITION OF THE TRIPLE CHAINS.

"I TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
TRESD, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
TV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
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Killen P.D., Burbelo P., Sakurai Y., Yamada Y.;
"Structure of the amino-terminal portion of the murine alpha 1(IV collagen chain and the corresponding region of the gene.";
J. Biol. Chem. 263:8706-8709(1988).
-I- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
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"Alpha 1(IV) and alpha 2(IV) collagen genes are regulated bidirectional promoter and a shared enhancer.";
proc. Natl. Acad. Sci. U.S.A. 85:9679-9682(1988).
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MEDLINE-89066738; Pubmed-3198626;
Kaytes P., Wood L., Theriault N., Kur
"Head-to-head arrangement of murine t
J., Biol. Chem. 263:19274-19277(1988).
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Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; Metazoa; Primates;
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                                                                   SEQUENCE OF 556-571.
TISSUE-Placenta;
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chain.";
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Kato I.;
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NCBI_TaxID=9606;
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         MEDLINE-92239022; PubMed-1571108;
Mann K.;
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Chem. 266:13124-13129(1991).
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the heparin-binding site
1035:139-145(1990).
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TREPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
OR 1548 (BY SIMILARITY).
OR 1551 (BY SIMILARITY).
OR 1652 (BY SIMILARITY).
OR 1665 (BY SIMILARI
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K., Okamoto N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No. 2.4e+02;
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                                                                                                                                                                                       of type V collagen.";
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         RT "MUTATIONS IN the COL5A1 gene are causal in the Ehlers-Danlos RT Syndromes I and II.";

RT Syndromes I and II.";

RT Ann. J. Hum. Genet. 60:547-554(1997).

RT Ann. J. Hum. Genet. 60:547-554(1997).

RT CC (FIBRILLAR FORMING COLLAGEN IS A MEMBER OF GROUP I COLLAGEN CC (FIBRILLAR FORMING COLLAGEN). IT IS A MINOR CONNECTIVE TISSUE CC (FOLLAGEN TO NEARLY UBIQUITOUS DISTRIBUTION. TYPE V COLLAGEN BINDS CC (FIBRILLAR FORMING COLLAGEN). IT IS A MINOR CONNECTIVE TISSUE CC (FIBRILLAR SULFATE, THROMBOSPONDIN, HEPARIN, AND INSULIN.

CC TO DUA, HEPARAN SULFATE, THROMBOSPONDIN, HEPARIN, AND INSULIN.

CC TO DUA, HEPARAN SULFATE, THROMBOSPONDIN, AND ONE ALPHA 2(V), CHAINS IN PLACENTA.

CC ONE ALPHA 3(V) CHAINS IN PLACENTA.

CC ONE ALPHA 3(V) CHAINS IN PLACENTA.

CC IPTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING CO.

CO ONE ALPHA 3(V) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

CC IPTM: PORTAL STATEMENT OF THE PRO-ALPHA 1(V) CHAIN ARE SULFATED.

CC IPTM: PORTAL STATEMENT OF THE PRO-ALPHA 1(V) CHAIN ARE SULFATED.

CC TYPE I (EDS1), A DISEASE CHARACTERIZED BY LOOSE-JOINTEDNESS AND CRACILLER, VELVETY, STRETCHABLE, BRUISABLE SKIN THAT HEALS WITH OR PROCULTAR TO ALPHA 3(V) AND ALPHA 1(XI) CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S16024;
MIM; 120215;
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MIM; 130010;
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[5]
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PIR; S03978; S03978.
PIR; S11303; S11303.
PIR; S16024; S16024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01410; COLFI; 1. Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT EDS1 SER-1639.
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Boutillon M.M., Bernillon J., Wallach
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1605 COLLAGE
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MEDILINE-8303946; PubMed-6291034;
Ou J.H., Rice C.M., Dalgarno L., Strauss E.G., Strauss J.H.;
Sequence studies of several alphavirus genomic RNAs in the region containing the start of the subgenomic RNA.";
Proc. Natl. Acad. Sci. U.S.A. 79:5235-5239(1982);
-1- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION.
-1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
BETWEEN THE CODONS FOR 1896-TYR AND 1897-LEU.
                                                                                                                                                                                                                                                                                                                               EMBL; J02363; AAA96: PIR; A03917; MNWVS. MEROPS; C09.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1429-2512 FROM N.A. MEDLINE-83299955; PubMed-6577423; Strauss J.H.; Strauss J.H.; "Sequence coding for the alphavirus nonstructural interrupted by an opal termination codon."; Proc. Natl. Acad. Sci. U.S.A. 80:5271-5275(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-54 FROM N.A. MEDLINE-83268700; PubMed-6308269; OU J.H., Strauss E.G., Strauss J.F. "The 5'-terminal sequences of the alphaviruses."; J. Mol. Biol. 168:1-15(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEÓUENCE FROM N.A.
MEDLINE-84148439; PubMed-6322438;
Strauss E.G., Rice C.M., Strauss J.H.;
"Complete nucleotide sequence of the g.
yirology 133:92-110(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NONSTRUCTURAL POLYPROTEIN (P2/U) [COMMANDED TO NSP4].
Sindbis virus (strain HRSP).
Viruses; ssrNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P03317;
21-JUL-1986
21-JUL-1986
15-DEC-1998
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NCBI_TaxID=11034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VGVLGRPG : |: || ||
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|IGIPGRPG 1108
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Rel. 37, Last annotation update)
POLYPROTEIN (P270) [CONTAINS: NONSTRUCTURAL PROTEINS
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NONSTRUCTURAL POLYPROTEIN (P270) (CONTAINS: N
                                                                                                                                                                                                                                                                                                                                                                                                                        (1)
SEQUENCE FROM N.A.
MEDLINE-91220725; PubMed-1673813;
MEDLINE-91220725; PubMed-1673813;
Shirako Y., Niklasson B., Dalrymple J.M.,
Shirako Y., Ockelbo virus genome an
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CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 SINDER VIRUSES.";
VIROLOGY 182:753-764(1991).

-I- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING RE-
-I- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE
-I- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR CODON UGA
BETWEEN THE CODONS FOR 1898-TYR AND 1899-LEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSP1 TO NSP4].
Sindbis virus (subtype Ockelbo
Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                          PROTEIN; RNA-binding; Helicase.
NONSTRUCTURAL PROTEIN NSP1.
NONSTRUCTURAL PROTEIN NSP2.
NONSTRUCTURAL PROTEIN NSP3.
NONSTRUCTURAL PROTEIN NSP4.
2 MW; 2F388CE32ACF5EDD CRC64;
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2; Mis
                                   Score 33; DB .
Pred. No. 3.6e
2; Mismatches
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NONSTRUCTURAL PROTEIN NSP4
MW; F3656FC8bB495726 CRC64
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viruses,
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3.6e+02;
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no DNA stage;
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Q1-JUN-1994 (Rel. 29, Created)
Q1-FEB-1996 (Rel. 33, Last sequence update)
Q1-OCT-2000 (Rel. 40, Last annotation update)
COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93338437; PubMed=1307247;
Christiano A.M., Rosenbaum L.M., Chung-Honet
Woodley D.T., Pan T.C., Zhang R.Z., Chu M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94327588; PubMed=8051117;
Christiano A.M., Greenspan D.S., Lee S., Uitto J.;
"Cloning of human type VII collagen. Complete primar
alpha 1(VII) chain and identification of intragenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA17_HUMAN
                                                            TISSUE=Placenta;
MEDLINE=94375010; PubMed=8088784;
                                                                                                                                                                                           "The carboxyl-terminal half of type VII collagenous NC-2 domain and intron/exon corresponding region of the COLTAl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parente M.G., Chung L.C., Ryynaenen J., Woodley D.T., Bauer E.A., Mattei M.-G., Chu M.-L., Uitto J.; "Human type VII collagen: cDNA cloning and chromosoma."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The large non-collagenous domain (NC-1) of type VII collagen is amino-terminal and chimeric. Homology to cartilage matrix protein, the type III domains of fibronectin and the A domains of von Willebrand factor.";
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                           Christiano
Uitto J., G
                                                                                                                                                                  corresponding region of the COL7 Hum. Mol. Genet. 2:273-278(1993)
                                                                                                                                                                                                                                                                  MEDLINE=93271985;
Greenspan D.S.;
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MEDLINE-9231902; PubMed-1567409;
Tanaka T., Takahashi K., Furukawa F., Imamura S.;
TMOLECULAr Cloning and characterization of type V
"Molecular cloning and characterization of type V
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Keratinocytes;
MEDLINE-92231902; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammon W.R., Abernethy M.L., Padilla K.M., Prisayanh P.S., Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III; "Noncollagenous (NCI) domain of collagen VII resembles multidomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gammon W.R., Abernethy M.L., Padilla K.M., Cook M.E., Wright J., Briggaman R.A., Hunt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human type gene.";
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                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular matrix.",
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  Jitto J., Greenspan D.S.
"Structural organization
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                                                                                                                            Q.
                         A.M., Hoffman G.G., Greenspan D.S.;
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PubMed=8499916;
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Catarrhini; Hominidae;
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                                                Chung-Honet L.C.,
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eson R.E.
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  gene (COL7A1),
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Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M., Uttto J., Pope F.M., Eady R.A.J.; "Clinicopathological correlations of compound heterozygous COL7A1 mutations in recessive dystrophic epidermolysis bullosa."; J. Invest. Dermatol. 107:171-177(1996).
                                                                                                                                                                                                                                                                                                                                                            VARIANTS RDEB AND DDEB.
VARIANTS RDEB AND DDEB.
MEDLINE=96220218; Pubmed-8644729;
Christiano A.M., McGrath J.A., Tan K.C., Uitto J.;
"Glycine substitutions in the triple-helical region of type VII collagen result in a spectrum of dystrophic epidermolysis bullosa and patterns of inheritance.";
                                                                                                     VARIANT RDEB ASP-2073.
MEDLINE-96310789; PubMed-8757758;
                                                                                                                                                Christiano A.M., McGrath J.A., Uitto J., "Influence of the second COL7A1 mutation in phenotypic severity of recessive dystrophic J. Invest. Dermatol. 106:766-770(1996).
                                                                                                                                                                                                                    VARIANT RDEB ARG-1782.
MEDLINE-96183562; Pubm
                                                                                                                                                                                                                                                                                  Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Uitto J., "Molecular basis of recessive dystrophic epidermolysis bullosa: genotype/phenotype correlation in a case of moderate clinical
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MEDLINE-96154068; Pub
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VARTANT DDEB SER-2040.
VARTANT DDEB SER-2040.
MEDLINE-94224777; PubMed-8170945;
Christiano A.M., Ryynaenen M., Uitto J.;
"Dominant dystrophic epidermolysis bullosa: identification of "Dominant dystrophic epidermolysis bullosa: identification of type VI"
"Dominant dystrophic epidermolysis bullosa: identification of type VI"
"Dominant dystrophic epidermolysis bullosa: identification of type VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Christiano A.M., Lee J.Y.-Y., Chen W.J., Laforgia S., "Prettbial epidermolysis bullosa: genetic linkage to (identification of a glycine-to-cysteine substitution helical domain of type VII collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cavalieri R., Uitto J.;
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MEDLINE-95164985; Pubm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT RDEB LYS-2798.

MEDLINE-93291877; PubMed-8513326;
Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,
Lin A.N., Dietz H.C., Hovnanian A., Uitto J.;
"A missense mutation in type VII collagen in two affected siblings
with recessive dystrophic epidermolysis bullosa.";
Nat. Genet. 4:62-66(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96081220;
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Jaervikallio A., Pulkkinen L., Uitto J.;
"Molecular basis of dystrophic epidermolysis
the type VII collagen gene (COL7Al).";
Hum. Mutat. 10:338-347(1997).
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pe VII collagen in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of more exons than any previously characterized gene."; 21:169-179(1994).
                                                                                                                                                                                                                 PubMed-8618018;
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Lee J.Y.-Y., Chen
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inant dystrophic epidermolysi
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This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
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I PYNE PROLINES AT THE THIRD POSITION OF THE TRIPEPTICE REPEATING INTT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

PROLINES AT THE THIRD POSITION OF THE TRIPEPTICE REPEATING INTERPRED PROCESSIVE DYSTROPHIC CHARACTERIZED BY TISSUE SEPARATION WITHIN THE DERMAL-EPIDERMAL MANESTS THE CLEAVAGE WITHIN THE PAPILLARY DESURS BELOW THE DOMINANT AND RECESSIVE INHERITANCE PAPILLARY DESURS BELOW THE BASAL DOMINANT AND RECESSIVE INHERITANCE PAPILLARY DESURS BELOW THE BASAL DOMINANT AND RECESSIVE INHERITANCE PAPILLARY DESURS BELOW THE BASAL DOMINANT AND RECESSIVE INHERITANCE PAPILLARY DESURS BELOW THE BASAL DOMINANT AND RECESSIVE INHERITANCE PAPILLARY DESURS BELOW THE BASAL DOMINANT BELISTERING SKIN DISEASE RESULTING FROM AUTONAMISED ACQUIRED BLISTERING SKIN DISEASE REFORM AUTONAMISED TO DISEASE: DEFECT IN COLTA1 IS A CAUSE OF DYSTROPHIC EPIDERMOLYSIS BULLOSA ACQUIRED RECESSIVE (RDEB). DEB IS A BLISTERING SKIN DISEASES WITH EITHER AND INHERITANCE. ULTRASPROCTURALLY, DEB IS CHARACTERIZED BY TISSUE MEMBRANE AT THE LEVEL OF THE ANCHORING FIBRILS. THE MOST SEVERE FORM OF ROBB IS THE LALLOPEAN-SIEWENS TYPE (HS-RDEB), A MILDER FORM OF ROBB IS THE HALLOPEAN-SIEWENS TYPE (HS-RDEB), A MILDER FORM OF ROBB IS THE HALLOPEAN-SIEWENS TYPE (HS-RDEB), A MILDER AND THE LOCALIZED TYPES (CLINICALLY, BROWS STRUCTURES, CORNEAL EROSIONS, SQUAMOUS CELL CARRING, WITH JOINT CONTRACTURES, CONTRAL EROSIONS, SQUAMOUS CELL CARRING AND PROPENSITY TO FORMATION OF CUTANEOUS SQUAMOUS CELL CARRING AND LESS REQUENT EXTRACTUREDUS OF THE WITH EXCESSIVE THE DOCKAYNES PROBUSED. THERE ARE SYULTANEOUS STRUCTURES CONTRAL EROSIONS, SQUAMOUS CELL CARRING AND LESS REQUENT EXTRACTUREDUS OF THE WITH EXCESSIVE THE COCKAYNES.

SQUAMOUS CELL CARRING AND LESS REQUENT EXTRACUTANEOUS HARD TYPE (CT-DDEB), AND PRETIBIAL EPIDEOUS HARD TYPE (T-DDEB) AND PRETIBIAL EPIDEOUS STRUCTURES (CKAYNES PERCUENT). THE PASINI TYPE (P-DDEB) WHICH IS SEVERE, THE LOCAL IS SEVERE, THE COCKAYNES.
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"Characterization of 18 new mutations in Court of the co
                                                                            2 GVLGRPG
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Hovnanian A., Rochat A., Bodemer C., Pe
Fraitag S., Christiano A.M., Uitto J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formation.";
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OF TO 513 DUE TO A FRAMESHIFT.
    GVAGRPG
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SUBUNIT: HOMOTRIMER.
                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TION: REF.5 SEQUENCE DIFFERS FROM THAT TO 523 DUE TO A FRAMESHIFT.
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IN POSITIONS
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LL11_HUMAN

ID RL11_HUMAN

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ID RL12;

AC P39026; P25121;

DT 01-MAY-1992 (Rel. 22, Created)

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Best Local Similarity 100
Matches 6; Conservative
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SEQUENCE
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human), and Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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"Evaluation and characterization of a porcine small intestine cD
library: analysis of 839 clones.";
Mamm. Genome 7:509-517(1996).
-I- FUNCTION: PROBABLY ASSOCIATES WITH 5S RNA.
-I- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
  SPECIES-Human;
Bhat K.S.;
                                                                                         "Cloning and determination of the primary structure of DNA complementary to the mRNA of human ribosomal protein L11."; Bicorg. Khim. 21:158-160(1995).
                                                                                                                                                                                             SPECIES-Human;
MEDLINE-95267091; PubMed-7748210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002132;
Pfam; PF00281; R1boSomal_L5; 1.
Pfam; PF00673; R1boSomal_L5_C; 1.
PROSITE; PS00358; RIBOSOMAL_L5; 1.
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MEDLINE-96327607; PubMed-8672129;
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15-DEC-1998 (Rel. 37, Last annotation update)
60S RIBOSOMAL PROTEIN L11 (FRAGMENT).
                                                                                                                                                                                      Mishin V.P.,
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                SEQUENCE FROM
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100.0%; Pr
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Г.
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annotation update)
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Search completed: June 13, Job time: 528 sec

2001, 14:30:38

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Best Local :
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EMBL; X62146; CAA44072.1; -.
PIR; S17351; R5RT11.
PIR; S45049; S45049.
PIR; JT0606; JT0606.
MIM; 604175; -.
                                                                                                                                     CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as to content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chan Y.-L., Olvera J., Paz V., Wool I.G.;
"The primary structure of rat ribosomal protein L11.";
Blochem. Blophys. Res. Commun. 185:355-362(1992).
-!- FUNCTION: PROBABLY ASSOCIATES WITH 5S RNA.
-!- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome
[4]
                                                                                                                                                                                                 Pfam; PF00281; Ribosomal_L5; 1. Pfam; PF00673; Ribosomal_L5_C; 1. PROSITE; PS00358; RIBOSOMAL_L5; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kenmochi N., Kawaguchi T., Rozen S., Davis E. Hudson T.J., Tanaka T., Page D.C.;
"A map of 75 human ribosomal protein genes.";
                                                                                                               SEQUENCE
                                                                                                                          CONFLICT
                                                                                                                                                                          Ribosomal protein; rRNA-binding INIT_MET 0 0
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132 VLGRPG
                       3 VLGRPG
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                                               Similarity 6; Conserv
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Perfect score:
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Ognym2 homo sapien
Ogxan8 streptomyce
O05848 mycobacteri
Ogugr5 homo sapien
Ogygr6 homo sapien
Ogy515 homo sapien
Ogy516 mycobacteri
Ogky13 streptomyce
Og2845 homo sapien
Ogv180 drosophila
O26639 strongyloce
O30764 streptomyce
O44989 caenorhabdi
O19979 caenorhabdi
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097409 anopheles g
033954 streptomyce
Q9ryk3 deinococcus
Q9sda5 arabidopsis
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| 40 | | | 3 | 42 | 41 | | | | 37 | | | | <u>ω</u> | 32 | ω | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| Ø90103 | 000407 | 201030 | 088207 | Q15094 | Q9KIZ8 | Q9L8C8 | Q90941 | 057539 | Q9JLC4 | Q9QY21 | Q9M285 | P71076 | Q9N281 | P74569 | Q13896 | Q9W327 | Q9K296 | Q9Z8B9 | Q22183 | Q9RK14 | Q9NZQ6 | Q9JLI2 | Q9JI04 | Q9W750 | Q9IAR8 | Q9XIC4 |
| עשן זיט ומרנטש ווטוי | | | O88207 mus musculu | Q15094 homo sapien | | Q918c8 sorangium c | Q90941 gallus gall | | Q9jlc4 mus musculu | | Q9m285 arabidopsis | P71076 bacillus su | | P74569 synechocyst | Q13896 homo sapien | þ | chlamydia | Q9z8b9 chlamydia p | Q22183 caenorhabdi | | 7 | Q9jli2 mus musculu | Q9j104 rattus norv | Q9w750 salmo salar | Q9iar8 salmo salar | Q9xic4 arabidopsis |

ALIGNMENTS

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Q06452
Q06452
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
EXTRACELLULAR MATRIX PROTEIN EMF1 ALPHA.

COLF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
EMBL; X69818; CAA49472.1; -.
INTERPRO; IPRO00087; -.
PFAM; PF01391; COLlagen; 13.
EXTRACELLULAR MATRIX.
SEQUENCE 812 AA; 72280 MW; 326573F37E46D50F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-94047120; PubMed-8230249;

Exposito J.Y., Van der Rest M., Garrone R.;

"The complete intron/exon structure of Ephydatia mulleri fibrillar

"The complete intron/exon structure of the evolution of an ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydatia muelleri (Mueller's freshwater sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
Haplosclerida; Spongillidae; Ephydatia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene module.";
J. Mol. Evol. 37:254-259(1993)
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                                                                                                                                                                                                                      203 VGALGRPG 210
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                                 PRELIMINARY;
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INTERPRO; IPRO00794;
INTERPRO; IPRO01927;
INTERPRO; IPRO01927;
INTERPRO; IPRO0193;
INTERPRO; IPR002106;
INTERPRO; IPR002198;
INTERPRO; IPR00106; adh.short; 1.
PFAM; PF00106; ketcacyl-synt; 3.
PFAM; PF0010698; Acyl_transf; 3.
PFAM; PF005098; Acyl_transf; 3.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.
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Matches 6
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DeHoff B.S., Sutton K.L., Roste
Submitted (NOV-1996) to the EME
EMBL; U78289; AAB6504.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces fradiae.
Streptomyces fradiae.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
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STRAIN-GASUA; TISSUE-SALIVARY GLAND;
MEDLINE-99145581; pubmed-9990055;
Arca B., Lombardo F., de Lara Capurro M., della Torre A.,
Prapping cons. James A.A., Coluzzi M.;
Prapping cons. encoding secreted proteins from the salivary glands the malaria vector Anopheles gambiae.";
Proc. Natl. Acad. Sci. U.S.A. 96:1516-1521(1999).
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STRAIN-GASUA; TISSUE-SALIVARY GLAND;
Arca' B., Lombardo F., Capurro de Lara Guimaraes M., della Torre A.,
Dimopoulos G., James A.A., Coluzzi M.;
"Trapping CDNAs encoding secreted proteins from the salivary glands
the malaria vector Anophales gambiae.";

Line malaria vector Anophales Sambiae.";
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Anopheles.
NCBI_TaxID=7165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sutton K.L., Rosteck F.R. J. Sutton K.L., Rosteck F.R. Sutton F.R. Sutton F.R. Sutton F.R. Sutton F.R. Sutton F.R. Sutton 
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 11, Last annotation update)
PRECURSOR (GSG3 PROTEIN PRECURSOR).
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5, Last sequence update)
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70001LE AND MODULES 1 & 2.
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Streptomycetaceae; Streptomyces
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE
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Bacteria; Thermus/Deinococcus
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PS00455; AMP_BINDING; UNKNOWN_1.
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RA Fijii C.Y., Mason T.M., Bowman C.L., Baristead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RI Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RI Nature 402:761-768(1999).
DR INTERPRO; IPRO00157; -.
DR INTERPRO; IPRO00151; -.
DR INTERPRO; IPRO01611; -.
DR INTERPRO; IPRO01611; -.
DR PFAM; PP00581; NB-ARC; 1.
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ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Nishikawa T., Nagai K., Sugiyama S., Ishibashi T., Fujimo Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishil S., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagah Masuho Y., Kanehori K., "NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AKO01507; BAA91728.1;

SEQUENCE 306 AA; 33028 MW; 649E417571F59E64 CRC64;
Q9XAN8;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CDNA FLJ10645 FIS, CLONE NT2RP2005767, MODERATELY S
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                           T., Fujimori K
, Ishii S., Kaw
a Y., Nagahari
                                                                                                                                                                                             1;
                                                                                                                                                                                                                                    Length 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki Y.,
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005848
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          X MEDLINE-98255987; PubMed-9634230;
A COle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston T., Taylor K., Whitehead S., Barrell B.G.;
T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
I Nature 393:537-544(1998).
E "MURPSCHITTE", BAJ218.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                           O05848 PRELIMINARY; PF
O05848 PRELIMINARY; PF
O05848-1997 (TrEMBLrel. 04, Crea
01-JUL-1997 (TrEMBLrel. 04, Last
01-CCT-2000 (TrEMBLrel. 15, Last
HYPOTHETICAL 34.5 KDA PROTEIN.
RV3218 OR MTCY07D11.08C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
PUTATIVE INTEGRAL MEMBRANE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A. Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol 21:77-96(1996).

EMBL; AL079355; CAB45566.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seeger S., Harris D.;

"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUTATIVE INTEGRAL SC4C6.02C.
                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
James K.D., P
                                                                                                                                                                                                                                                                             STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                              Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 IGVLSRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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| (JUN-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            04, Created)
04, Last sequence up
15, Last annotation
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the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Last sequence up, Last annotation PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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No.
                                                                                                                                                                                                                                                                                                                                                    Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 AA
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                                                                                                                                                                                                                                                                                                                                                                      Actinobacteridae;
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88;
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Length 317

Indels

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Gaps

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Mycobacterium.

Sulston

J.E.,

Holroyd

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Harris

D.,

and A:

physical map Cullum J.,

for

physical

for

Streptomyces

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Query Match
Best Local s
Matches 6
                                                                                                                             Submitted (DEC-1999) to the EMBL; AL049851; CAB63075.1, SEQUENCE 377
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Best Local s
Matches 6
                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DJbosca
DJB9J22B.1.
Homo sapiens (Human).
Homo rapiens (Human).
Homo sapiens (Chordata; Cr
horia; Primates; Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                   DJ889J22B.1.
                                                                                                                                                                                                                                                                                                                                                                             Q9UGR6;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UGR5;
01-MAY-2000
01-MAY-2000
01-MAY-2000
DJ889J22B.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steward C.;
Submitted (DEC-1999) to the
EMBL; AL049851; CAB63076.1;
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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PFAM; PF00781; DAGKC; 1:
PRODOM; PD005043; -; 1.
Hypothetical protein
SEQUENCE 321 AA; 34474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GVLGRPG 8
|:||||
|255 GLLGRPG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UGR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                     Similarity 85.7
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMLGRPG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVLGRPG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence update)
(TremBLrel. 13, Last annotation update)
(NOVEL PROTEIN (ISOFORM 1)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ıl protein.
321 AA; 34474
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                                                                  83.3%;
85.7%;
                                                                                                                              37053 MW;
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                                                                                                                                                                 the 5.1;
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85.7%;
                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
(ISOFORM 2)) (FRAGMENT)
                                                             Score 35;
Pred. No.
                                                                                                                                                                  EMBL/GenBank/DDBJ databases
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Pred. No.
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Catarrhini;
                                                                                                                           68234A527D009007
                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331
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                                              Indels
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                                     0;
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                 RX MEDLINE-9825987; PubMed-9634230;

R Cole S.T. Brosch R. Parkhill J. Garnier T., Churcher C., Harr Gordon S.V. Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy, A., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).

R TUBERCULIST; Rv1869C; ...

RR TUBERCULIST; Rv18601205; ...

RR TUBERCULIST; Note The Nature 1980 Control of the Nature 1980 Contr
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Best Local Similarity
Matches 7; Conserv
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INTERPRO; IPR000205; -.
INTERPRO; IPR001100; -.
PFAM; PF00070; pyr_redox;
                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
Bacteria; FirmLoutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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01-MAY-1997 (TIEMBLIEL 03, La
01-OCT-2000 (TIEMBLIEL 15, La
HYPOTHETICAL 43:6 KDA PROTEIN.
RV1869C OR MTCY359.04
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P95146;
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DJ682J15.1.
HOmo sapiens (Human).
Tharvota; Metazoa; Chordata; C;
Tharvota; Metazoa; Primates; C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collagen.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1999) to the EMBL; AL034452; CAB45235.1; INTERPRO; IPRO00087; PFAM; PF01391; Collagen; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DJ682J15.1 (NOVEL COLLAGEN TRIPLE HELIX REPEAT CONTAINING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Y515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VGVLGRPG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Catarrhini; Hominidae;
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Q92845;
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O1-FEB-1997 (TREMBLEGL. C
O1-JUN-2000 (TREMBLEGL. 1
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

MOI. Microbiol. 21:77-96(1996).

EMBL; AL356592; CAB92217.1; ...
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
ACBI_TaxID=1902;
                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rollodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Ra Harris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck J.,
Ra Harris N.L., Harvey D., Heimann T.J., Wei M.-H., Ibegwam C.,
Ra Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Ra Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Ra Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Ra Mcunto G., Milshina N.Y., Mobarry C., Morris J., Woshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Reison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Ra Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Welliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Zhao Q., Zheng L.,
Rather Y. H., Phong E. M., Thong W., Thong Y., Catte B.,
Rather Y. H., Phong E. M., Phong Y., Phong Y., Phong Y., Phong Y., Park Y., Phong Y., Park Y., Phong Y., Park Y
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RA Annanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
RA Annanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barley R.M., Baybayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Bouck J., Bokstein P., Brottlier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garo N.S., Gelbart W.M., Glasser K.,
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EMBL; U59919; AACS0788.1; -.
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1114
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Title: Perfect score: Sequence:

Scoring table:

Patent No. Sequence

Sequence

126,

Sequence Sequence

2, Appli 14, Appl 2, Appli 2, Appli 2, Appli 2, Appli 2, Appli 2, Appli 5, S240846

Sequence

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Sequence

2, Appli 2, Appli 2, Appli 17, Appl 2, Appli 2, Appli 6, Appli 6, Appli 2, Appli 4, Appli 4, Appli 14, Appli

Sequence Sequence Sequence Sequence

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protein -

Run on:

Minimum Maximum

DB seq

Post-processing:

Total number

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/laa/backfiles1.pep:*
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Maximum Match 100%
Listing first 45 s
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US-08-804-27C-8
US-08-804-198-2
US-08-964-617-4
US-08-964-617-4
US-08-961-897-421-6
US-09-318-528-6
US-09-318-528-6
US-09-318-528-6
US-09-107-248-9
US-08-801-263A-9
US-08-801-263A-9
US-08-415-593-41
US-08-81-843A-17-5
US-08-463-912-88-6
US-08-463-918-8
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         Sequence 2, Appli
Sequence 8, Appli
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Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 175, Appli
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Sequence 19, Appli
Sequence 12, Appli
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                                                                                                              COMPUTEK: ASCICOS COMPUTEK: ASCICOS) TEXT ON SOFTWARE: ASCICOS) TEXT ONLY CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/804,22 FILING DATE: FEDTUARY 21, 1997 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Plant, Thomas, G. REGISTRATION UMBER: 35,784
REFERENCE/DOCKET NUMBER: X-823
TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4472 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: unknown MOLECULE TYPE: protein
US-08-804-227C-2
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US-08-804-227C-2
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GENERAL INFORMATION:
                                                                     Query Match
Best Local s
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DeHOIF, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
LIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPDY disk
COMPUTER. TRM COMPATIBLE
             4155 GILGRPG 4161
                                           2 GVLGRPG
                                                                       Similarity 6; Conserv
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85.7%;
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ry 21, 1997
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US-08-136-742A-2
US-08-135-809A-2
US-08-466-886-17
US-08-469-461-2
US-08-469-461-2
US-08-469-461-2
US-08-459-552A-14
US-07-890-609-2
US-08-469-617-17
PCT-US93-11667-2
520486-55-22
US-08-469-617-17
PCT-US93-11667-2
US-08-494-168-2
US-08-494-168-2
US-08-494-168-2
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1; Mismatches
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2.9e+02;
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Result

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Score

Query Match

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ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION UNMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 31,7276-2459
INFORMATION FOR SEQ ID NO: 14:
LENGTH: 4545 AMINO acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
                                                                                                                                       ENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: KUNSCOSS, Stuart A.
APPLICANT: ROSteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                         08-804-227C-8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-804-227C-14
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                                                                                    CITY: INDIANAPOLIS STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: un
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              2 GVLGRPG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 85. es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08, FILING DATE: February 21, CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: INDIANAPOLIS STATE: IN
                                                                                                                                                                                                                                                                     8, Application US/08804227C
5. 5876991
                                                         46285
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                                                                     USA
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T: Kuhstoss, Stuart A.
T: Rosteck, Paul R., Jr.
T: Sutton, Kimberly L.
INVENTION: POLYKETIDE SYNTHASE GENES
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85.7%; Pred. No. 6
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ry 21, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4545;
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                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4550 amino acid
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                                                                                 ATTORREY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P911
TELECOMMUNICATION INFORMATION:
TREEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-804-198-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Plant, Theormas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-82:
TELECOMMUNICATION INFORMATION;
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4550 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.
Matches 6; Conservative
                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NAMES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4223 GLIGRPG 4229
                                                                                                                                                                                                                                                                         COMPUTER: Macintosh
OPERATING SYSTEM: M
                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                   CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                CITY: INDIANAPOLIS
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SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
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FILING DATE: Februe
CLASSIFICATION: 435
                                            i: 4550 amino acids amino acid
                  TYPE:
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INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08804198
                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuhstoss, Stuart A.
Rao, Nagaraja R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgett, Stanley G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    February 21,
                                                                                                                                                                                                                           US/08/804,198
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ry 21, 1997
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Sequence

tent No.

COUNTRY:

Query Match

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Query Match
Best Local Similarity
""" tches 6; Conserve
                                                                                                                                                                                                               Query Match
Best Local Similarity
Thehes 5; Conserve
                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-526-964-4
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                                                                                                                  US-08-946-617-4
                                                                                                                              RESULT
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                                                                                   Sequence 4, Application US/08946617 Patent No. 5869634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08526964 Patent No. 5698421
                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (216) 241-0816
NFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4223 GLLGRPG 4229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Guo, Huatao
APPLICANT: Yang, Jian
TITLE OF INVENTION: Nucleotide Integrase Preparation
NUMBER OF SEQUENCES: 17
                                                                                                                                                                       534 GILGKPG 540
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: GOLTICK, Mary E REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U:
ZIP: 44114
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                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                 2 GVLGRPG 8
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    INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohio
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800 Superior Avenue
                                                                                                                                                                                                                                                                                                                                                                                  785 amino acids
                                       Zimmerly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                      Lambowitz,
                                                                                                                                                                                                                                                                                                                                          linear
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85.7%;
Nucleotide Integrase Preparation
                                          Steven
                                                         Alan M
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1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                   Patent No. GENERAL I
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/031,897
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                             APPLICANT: Zimmerly, Steven
APPLICANT: Guo, Huatao
TITLE OF INVENTION: Methods Cleaving DNA with Nucleotide
TITLE OF INVENTION: Integrases
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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534 GILGKPG 540
                                                                                                                                                                         CITY:
STATE:
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                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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OPERATING SYSTEM:
                              FILING DATE
                                                                                                                                              ZIP:
                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
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               CLASSIFICATION
                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                               44114
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5; Conserv
                                                                                                                                                                           Ohio
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                                                                                                                                                                                                    800 Superior Avenue, Suite 1400
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    Lambowitz, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                    Calfee, Halter & Griswold
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                                                                                                              Floppy disk
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71.4%;
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Pred. No. 1.8e+02;
2; Mismatches 0;
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NAME: Docherty, Pame. REGISTRATION NUMBER:

Pamela A

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Query Match
Best Local Similarity
  78.6%;
85.7%;
    Score 33; DB 3;
Pred. No. 1.4e+05;
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APPLICANT:

Molnar, Istv Zirkle, Ross

Istvan

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Best Local Similarity
Thes 5; Conserv
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                                         ; MOLECULE TYPE: peptide US-08-689-421-6
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TELEFAX: (216)241 0816
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 9-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 60080290 NO. 6008029disk of No. 6008029th America,
STREET: 405 Lexington Avenue, 64th Floor
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HYPOTHETICAL:
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MEDIUM TYPE: Floppy disk
                                                                                                                                  SEQUENCE CHARACTERISTICS:
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534 GILGKPG 540
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STRANDEDNESS: single
TOPOLOGY: linear
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LECOMMUNICATION TOTAL
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                          TORNEY ASSETTINGTON, James J.
REGISTRATION NUMBER: 38,711
REGISTRATION NUMBER: 4554.204-WO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GVLGRPG 8
                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                       TOPOLOGY:
                                                                                                    TYPE: amino acid
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                                                                                                                  LENGTH:
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10174-6401
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PURIFIED COPRINUS LACCASES AND NUCLEIC ACIDS
ENCODING SAME
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Pred. No.
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. 1.8e+02;
0;
DB 3; Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Thes 6; Conserv
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; MOLECULE TYPE:
US-09-389-528-6
                                                                                                                                                           RESULT 10
US-09-335-409-4
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                                                                GENERAL
                                                                                           Sequence 4, Application US/09335409 Patent No. 6121029
APPLICANT: Schupp, Thoma APPLICANT: Ligon, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08
FILING DATE: 9-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: "TOTALE TATALE TATAL
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 405 Le:
CITY: New York
                                                                                                                                                                                                                                                                                       2 GVLGRPG 8
|||| ||
1 GVLGNPG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 212-878-9655
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                                                                INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Halkier, Torben P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown,
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Brown, Kimberley M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212-867-0123
                                 Thomas
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PURIFIED COPRINUS LACCASES AND NUCLEIC
ENCODING SAME
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4e+05;
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CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES FILE REFERENCE: 4-30582A

APPLICANT: Cyr, Devor APPLICANT: Goerlach,

Devon

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; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-335-409-4
                                                                                                                                   ; MOLECULE TYPE: protein US-08-801-263A-2 ·
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                                                   Matches
                                                                Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                              TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0 EQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JOHNSLOW, APPLICANT: Davis, Nancy L. APPLICANT: Davis, Nancy L. APPLICANT: Simpson, Dennis A. APPLICANT: Simpson, Dennis A. APPLICANT: Simpson, Dennis A. TITLE OF INVENTION: System for the In vivo Delivery and TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
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| 1578 VGLLGSPG 1585
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
STREET: 1211 East Morehead Street
                                               Local Similarity
nes 5; Conserv
                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                             NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 54
                                                                                                                                                                    TOPOLOGY:
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1 VGVLGRPG 8
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No. 5811407th Carolina
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62.5%;
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75.0%;
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                                               Score 33; DB
Pred. No. 8.1e
2; Mismatches
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Pred. No.
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8.1e+02;
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                                            Indels
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Best Local S
Matches 5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2500 amino acid
TYPE: amino acid
                         NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                     APPLICANT: Davis, Nancy L.

APPLICANT: Simpson, Dennis A.

TITLE OF INVENTION: System for the In Vivo Delivery and TITLE OF INVENTION: System for the Tourist State of Tourist S
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APPLICATION NUMBER: US 0
FILING DATE: 19-FEB-1997
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VGVLGRPG 8
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1211 East Morehead Street
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                                                                                                                                                                                                                                                                                     Johnston, Robert E.
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Pred. No.
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                                                                                                                                            the Bone Marrow
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA REPLACATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

STATE: 1

No. 5811407th Carolina

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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Applic Patent No. 6008035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/801,263A FILLING DATE: 19-FEB-1997 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,248
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-147
TELECOMMUNICATION INFORMATION:
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2512 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         722 IGVIGTPG 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   CITY: Charlotte
STATE: No. 6008035th Carolina
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                                                      NAME: Sibley, Kenneth D.
                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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1211 East Morehead Street
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                                                                                                                US 08/801,263
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Pred. No. 8.
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Search completed: June 13, 2001, 14:27:08

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Query Match
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US-08-801-263A-5
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                                                                                                                                      ; TOPOLOGY: 11; MOLECULE TYPE: US-08-801-263A-5
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                                                             Matches
                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2517 amino acids
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Simpson, TITLE OF INVENTION:
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722 IGVIGAPG 729
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                              NAME: Sibley, Kenneth REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 19-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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System for the In Vivo Delivery and
Expression of Heterologous Genes in
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62.5%;
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Pred. No.
                                                                            Score 33; DB 2;
Pred. No. 8.2e+02
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                                                             Mismatches
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Perfect score:
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/SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                    Length
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                                R85659
Y79129
Y79129
W07623
W94929
W27314
W45521
Y02457
Y79132
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                                                                                                                                                   Mastitis vaccine p
Mastitis vaccine m
Peptide antagonist
N-terminal peptide
US5864028 sequence
Human prostate ass
Glyceraldehyde-3-p
Fragment of glycer
Human foetal brain
Human lung tumour
Human lung tumour
                                                                                                                                                                                                                                                                                                                 Description
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| 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 38 | 38 | 38 | 38 | 38 | 38 |
| 6 | σ | g | σ | 9 | g | 9 | 9 | 9 | S | 9 | σ | σ | S | 6 | 6 | 9 | 6 | 6 | 9 | σ | 6 | g | σ | 6 | ð | σ | ð | æ | 8 | æ | 88.4 | 88.4 | 88.4 |
| 336 | 336 | 336 | 335 | 335 | 334 | 334 | 333 | 333 | 333 | 238 | 175 | 174 | 171 | 160 | 156 | 149 | 139 | 136 | 135 | 133 | 130 | 107 | 93 | 70 | 47 | 39 | 31 | 340 | 335 | 335 | 268 | 127 | 127 |
| 22 | 20 | 15 | 20 | 11 | 21 | Ξ | 21 | 21 | 19 | 21 | 21 | 21 | 21 | 18 | 20 | 21 | 18 | 21 | 21 | 21 | 21 | 21 | 21 | 14 | 21 | 14 | 19 | 20 | 20 | 20 | 20 | 21 | 20 |
| Y85681 | Y35244 | R56486 | Y28472 | R05284 | Y55844 | R03211 · | B19021 | в19020 | W55089 | B28132 | G28442 | G35522 | G22592 | W14722 | Y06889 | G35523 | W27835 | G54490 | _ | G33938 | G44842 | G19017 | G34299 | R40212 | G15911 | R38788 | W53450 | Y14930 | Y05368 | Y07036 | Y14921 | B44447 | Y29540 |
| treptococcal pla | moniae pr | min receptor. | ldehy | o acid s | P. ciferrii glycer | Amino acid sequenc | Amino acid sequenc | | | Glyceraldehyde-3-p | Arabidopsis thalia | Arabidopsis thalia | Zea mays protein f | C. hirsutus GPD. | aureus glyceral | Arabidopsis thalia | Amino acid sequenc | Zea mays protein f | Zea mays protein f | Arabidopsis thalia | Zea mays protein f | brd | ŝ | _ | rabidopsis | tococ | obacterium | acid sequen | HCMV induci | t cance | o acid | n lung | Human lung tumour |

ALIGNMENTS

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RESULT
R85657
WPI; 1995-185598/24
            Scheifinger CC, Smiley DL;
                                       05-NOV-1993;
                                                    04-NOV-1994;
                                                                 11-MAY-1995
                                                                             W09512410-A1
                                                                                                                                         Synthetic.
                                                                                                                                                                                19-JAN-1996 (first entry)
                                                                                                                                                                                               R85657;
                                                                                                                                                                                                           R85657 standard; peptide; 22 AA.
                          (ELIL ) LILLY & CO ELI.
                                                                                                 Modified-site
                                                                                                                      Modified-site
                                                                                                                                                      Mastitis vaccine peptide; microbial adherence.
                                                                                                                                                                   Mastitis vaccine peptide.
                                       93US-0147765
                                                    94WO-US12752
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                                                                                                       Location/Qualifiers
                                                                                          /note= "C-terminal hydroxy group"
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R85659
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Best Local Similarity 8/...
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         R85659 is a mastitis vaccine multiple antigen presentation peptide, identified using a new method for identifying molecules responsible for microbial adherence.
                                                                                              Claim 4; Pages 26-27; 32pp;
                                                                                                                Identifying molecules responsible for microbial adherence - used partic. for identifying new mastitis vaccine peptide(s) and multiple antigenic presentation peptide(s).
                                                                                                                                                                                                          WPI; 1995-185598/24.
                                                                                                                                                                                                                                                   Scheifinger
                                                                                                                                                                                                                                                                                (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                       05-NOV-1993;
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                                                                                                                                                                                                                                           Smiley DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= OTHER
/note= "3 ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "the omega amino gp. is acylated with the ... Peptide R85657"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abel-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "the omega amino gp. is acylated with the peptide R85657 via an additional C-terminal Lys residue (the omega amino gp. of which is also acylated with the peptide R85657)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               amino propionic acid
                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 16
Pred. No. 0.13;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identified using a new m
for microbial adherence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 22;
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DE XX KW XX XX XX PN PN XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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blid to a zonula occludens toxin (207) receptor, yet do not care physiologically modulate the opening of mammalian tight junctions and human zonulins, which is believed to be critical for receptor and human zonulins, which is believed to be critical for receptor combinant DNA techniques. The present peptide antagonist are based on a common motif of zor creombinant DNA techniques. The present peptide antagonist is used in a claimed method for treatment of a condition associated computed in the brain. It can be used for treatment of a condition associated computed is the brain but does not modulate the opening of my condition associated computed is the brain but does not modulate the opening of my condition associated computed is set to the convulsive setzure, chemical toxins, uraemia, meningitis, encephalomyelitis, e.g. infective, or bacterial or convulsive setzure, traumatic brain injuries, radiation brain injury, constructive, or democratic period diseases, e.g. multiple constructions or Guillian-Barre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Y79129
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide antagonist of zonulin useful as antiinflammatory agent for treating cerebral ischemia, stroke, cerebral edema, gastritis, shigeilosis, viral gastroenteritis, meningitis, encephalomyelitis .
                                                                                                                                                                                                                                                                                                                                                                                                                one of 25 such pe
bind to a zonula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 52; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-205565/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zonulin; antagonist; zonula occludens toxin receptor; blood-brain barrier; antiinflammatory; cerebroprotecti neuroprotective; dermatological; antiulcer; antiviral; antibacterial; cytostatic; anti-HIV; vulnerary; antial hypotensive; immunosuppressive; antiparasitic; vasotrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200007609-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide antagonist of zonulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y79129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y79129 standard; Peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                      s present sequence is that of a peptide antagonist of zonulin, of 25 such peptides (see Y79105-29) of the invention that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VDGFGRIG 8
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AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy.
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87.58;
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Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiparasitic; vasotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
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RESULT
W94929
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W07623
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Best Local S
Matches 7
                                                                                                                                      Query Match
Best Local
                                                                                                                               Matches
                                                                                                                                                                                                   This sequence represents the N-terminal peptide of GAPDH. GAPD blinds to a sequence found in anti-tumour necrosis factor-alpha (TNF-alpha) ribozymes. The binding of GAPDH acts to stabilise ribozyme and has the ability to stimulate cleavage activity of hammerhead ribozymes. This increase is most likely due to the
                                                                                                                                                                                                                                                                                      Tumour necrosis factor-alpha ribozymes - useful to treat disorders associated with TNF-alpha overexpression, e.g. rheumatic arthritis,
        06-MAY-1999
                           W94929;
                                            W94929 standard;
                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               WO9639499-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozyme; tumour necrosis factor-alpha; rheumatic arthritis; AIDS; autoimmune disease; TNF-alpha; viral disease.
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                   WPI; 1997-043121/04.
                                                                                                                                                                                                                                                                                                                                      Sioud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W07623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W07623 standard;
                                                                                                                                                                                             destabilisation
                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENE
                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1996.
                                                                                           G
                                                                                                  1 VDGFGRIG 8
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| vngfgrig
                                                                                         vngfgr1g
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                                                                                                                                                                                                                                                                              or autoimmune disease
                                                                                                                                       Similarity
                                                                                                                                                                                                                                                           2; Page 61; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
7; Conser
                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide of
                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                      SHEARS PTY LTD
       (first entry)
                                                                                          12
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                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                          96WO-AU00339
                                           peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.48;
                                                                                                                                      88.4%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAPDH.
                                                                                                                                                                                             duplex
                                                                                                                             Score 38; DB
Pred. No. 0.39
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 21;
Pred. No. 3.2e+05;
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                                                                                                                                     DB 18;
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                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8;
                                                                                                                              Indels
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                                                                                                                                                                                                                                         GAPDH
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                                                                                                                              Gaps
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RESULT
W27314
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-1992;
03-NOV-1993;
05-JUN-1995;
          diagnosis;
                       Human; prostate cancer; immunotherapy; therapy; immunodiagnosis;
                                                    Human prostate associated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 51-52; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stabilising RNA by attachment to specific second RNA sequence improving activity of ribozymes or antisense molecules or for improving polypeptide production from mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-131361/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNF-alpha; ribozyme; growth hormone; blood factor; enzyme; vaccine; virus; tumour necrosis factor; rheumatodd arthritis; septic shock; acquired immune deficiency syndrome; graft vs. host disease; cachexia; immune dysfunction; Alzheimer's disease; psoriasis; leukaemia; cancer;
                                                                                  27-APR-1998
                                                                                                              W27314;
                                                                                                                                             W27314 standard;
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sioud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA stabilisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5864028 sequence ID #33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1995;
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                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                               1 VDGFGRIG
                                                                                                                                                                        6
                                                                                                                                                                                                                   vngfgrig
                                                                                                                                                                                                                                                                            Similarity 7; Conserv
            vaccine;
                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                            Conservative
                                                                                 (first entry)
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93WO-AU00567.
95US-0464073.
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                                                                                                                                             Peptide; 18
          antibody; human
                                                                                                                                                                                                                                                                                        88.4%;
                                                                                                                                                                                                                                                                          : Score 38; DB
: Pred. No. 0.39
1; Mismatches
                                                                                                                                             3
                                                                                                                                                                                                                                                                                  DB .
                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                       Length 12;
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or designed
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RESULT
W45521
ID W4
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                                                                                                                                                                                                                                                                                                                                                                                                     characteristics prostate adenocarcinoma cell line inclap. Egg (ATCC CRL 1740) with human prostatitis sera. Comparison of the peptide sequences with database sequences revealed homology peptides not previously associated with human prostate. These were glyceraldehyde-3-phosphatate dehydrogenase (see W27316), alpha-human fructose biphosphate aldolase (see W27317), calreticulin (see W27318 and W27319), malate dehydrogenase (see W273120) and cystic disease fluid protein (see W27312 and W27313). Immunogenic portions of these peptides can be used in a claimed pharmaceutical composition for the treatment of prostate cancer, in a claimed vaccine for treatment of prostate cancer, or used to raise a monoclonal or polyclonal antibody useful in claimed methods or prostate cancer. 17 HPA polypeptides (see W23312-23 and W27303-07) and 14 other immunogenic polypeptides (see W23312-23 and W27303-07)
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Misc-difference
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15-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-470816/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 Peptides (W27314 and W27315) were obtained following screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic portions of prostate proteins - useful to develop products to detect, monitor, treat or inhibit development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                         Glyceraldehyde-3-phosphate dehydrogenase N-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                   Glyceraldehyde-3-phosphate dehydrogenase; GAPDH; polyglutamine;
CAG repeat domain; neurodegenerative disorder; inhibition;
                                                                                                                                                                W45521;
                                                                                                                                                                                          W45521 standard; peptide;
                         Homo sapiens
                                               CAG repeat domain; neurodegenerative disorder; in Huntington's disease; schizophrenia; psychiatric
                                                                                                                                     27-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                       1 VDGFGRIG
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| vngfgrig
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DG
                                                                                                                                                                                                                                                                                                                 Similarity
7; Conser
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                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                             14
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96US-0616745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84pp; English.
                                                                                                                                                                                                                                                                                                                                88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Twardzik DR;
                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                  Score 38; DB Pred. No. 0.59
1; Mismatches
                                                                                                                                                                                                                                                                                                                                  DB 18;
0.59;
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                             Length 18
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT
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  Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the N-terminal sequence of glyceraldehyde-3-phosphate dehydrogenase (GAPDH). The invention relates to a new screening assay for compounds capable of inhibiting binding of GAPDH to polyglutamine. The assay comprises providing an aqueous solution containing a test compound, polyglutamine-containing molecules and GAPDH and determining if binding of GAPDH to the polyglutamine-containing molecules is reduced in the presence of the test compound. Inhibitors identified by the above assay could be used to treat neurodegenerative diseases or psychiatric disorders caused by a gene containing an extended CAG domain, e.g. Huntington's disease or schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening assay for inhibitors of GAPDH binding for use in treating neuro-degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burke JR, Enghild J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Column 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                      N-terminal; prostate tumour cell; immunogenic; treatment; diagnosis; prostate cancer; glyceraldehyde-3-phosphate dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                         Fragment of glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                 13-JUL-1999
                                                                                                                                                                                                                                                                                                        Y02457;
                                                                                           23-JUN-1998;
07-OCT-1997;
                                                                                                                                                                                                                                                                                                                              Y02457 standard; Peptide; 18
New isolated prostate polypeptides useful for the treatment,
                        WPI; 1999-277272/23.
                                                                                                                            07-OCT-1998;
                                                                                                                                                     15-APR-1999.
                                                                                                                                                                           WO9918210-A2
                                                                                                                                                                                                  Homo sapiens
                                                                    (CORI-) CORIXA
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                                                                                                                                                                                                                                                                                                                                                                                                1 VDGFGRIG 8
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                                                                                                                                                                                                                                                                                                                                                                                     vngfgrig
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                              Mitcham
                                                                                                                                                                                                                                                                                 (first entry)
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                                                                     CORP
                                                                                           98US-0102679
97US-0946026
                                                                                                                               98WO-US21166
                                                                                                                                                                                                                                                                                                                                                                                                                                                88.4%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strittmatter WJ,
                                                Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB Pred. No. 0.59
1; Mismatches
                                                SG
                                                Twardzik DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vance
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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psychiatric
                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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RESULT
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Best Local
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The present sequence is that of the N-terminal region of foetal human brain zonulin. The N-terminal sequences of human adult and foetal zonulins (see Y79130-36) were compared with Vibrio cholerae zonula occludens toxin (207) to identify a common motif thought to be involved in receptor binding. Peptide antagonists (see Y79105-29) based on this motif are useful as antiinflammatory agents for treatment of gastrointestinal inflammation, and for treatment of conditions associated with breakdown of the blood-brain treatment of conditions associated with breakdown of the blood-brain treatment of conditions associated with breakdown of the blood-brains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the N-terminal of a human glyceraldehyde-3-phosphate dehydrogenase. The specification polypeptides and DNA which are obtained from prostate tumour cells. The polypeptide comprises an immunogenic portion of a
                                                                                                                                                  New peptide antagonist of zonulin useful as antiinflammatory agent treating cerebral ischemla, stroke, cerebral edema, gastritis, shigellosis, viral gastroenteritis, meningitis, encephalomyelitis
                                                                                                                                                                                                                                                                                            03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate protein. The polypeptides and DNA obtained from prostate tumour cells, as well as antibodies raised against the protein, compared in the treatment, diagnosis and monitoring of prostate
                                                                                                                          Example 4; Fig 7; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis and monitoring of prostate cancer
                                                                                                                                                                                                            WPI; 2000-205565/18
                                                                                                                                                                                                                                                                 (UYMA-) UNIV
                                                                                                                                                                                                                                                                                                                        28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                             WO200007609-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zonulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y79132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y79132 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vngfgrig 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n; antagonist; zonula occludens toxin receptor; blood-brain barrier; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 87.177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                  MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                        99WO-US16683
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     /note= "unidentified residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zonulin N-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.4%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB Pred. No. 0.59
1; Mismatches
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ງ.59;
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Query Match
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Matches 7
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23-JUL-1998;
23-JUL-1998;
                                                                                                                                                                                                                                                                                                                       22-DEC-1998;
28-JAN-1998;
28-JAN-1998;
                                                                                   The present invention describes lung tumour specific polynucleotides and tumour antigens. 207144 to 207246 and 208301 to 208325 represent specifically claimed polynucleotides, and Y29486 to Y29571 represent amino acid sequences from the present invention. The lung tumour specific polynucleotides and polypeptides can be used in pharmaceutic compositions and vaccines to inhibit the development of lung cancer. They can also be used to detect lung cancer in a patient. Probes and
                                                                They can also be used to detect lung cancer antibodies derived from the lung tumour sequentection of lung cancer.
                                                                                                                                                               Example 3; Page 114; 171pp; English.
                                                                                                                                                                                  Lung tumour specific polynucleotides of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lung
                                                Sequence
                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                            Frudakis TN,
                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                   WO9938973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lung tumour protein L86S-49 predicted amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y29539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y29539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   barrier
                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                 18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                               26-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         immunotherapy;
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DB; Z07223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conserv
                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                            Lodes
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                                                                                                                                                                                                                                                                                98US-0040828.
98US-0040831.
98US-0122191.
98US-0122192.
                                                                                                                                                                                                                                                                                                                       98US-0219245.
98US-0015022.
98US-0015029.
                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                         nour protein; therapy; diagnosis;
detection; inhibition.
                                                                                                                                                                                                                                                                                                                                                               99WO-US01642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 124
                                                                                                                                                                                                                                            Ľ,
          88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.4%;
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Pred.
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          38;
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                                                                                                                                                                                                                                            Reed
        DB
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0.73;
                                                                            sequences
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                   20;
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                   Length
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                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                            development
                                                                                                         pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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B44446
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                                                                                                                                                                                      Query Match
Best Local S
Matches 7
Human; lung tumour protein; therapy; diagnosis; lung cancer; vaccine;
                    Human lung tumour protein L86S-51 predicted amino acid sequence.
                                                 13-0CT-1999
                                                                                                                                                                                                                                                                     The present sequence is given in a specification relating to compounds for therapy and diagnosis of lung cancer. Polypeptides comprising at least an immunogenic part of a lung tumour protein are disclosed. The polypeptides are useful for inhibiting the development of cancer, especially lung cancer. Samples of T cells expressing the polypeptides may be used to inhibit the development of cancer. The polypeptides are also useful for detecting and monitoring the progression of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1999;
09-AUG-1999;
30-DEC-1999;
03-MAR-2000;
                                                                                       Y29540 standard; Protein; 127 AA.
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                               especially lung cancer.
                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 132; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 Novel lung tumor polypeptides and polynucleotides, useful detecting, monitoring or treating cancer, especially lung
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-638466/61.
                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; C79104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2000; 2000WO-US08560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lung tumour-specific antigen encoded by cDNA #57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2000
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                                                                                                                                                         1 VDGFGRIG 8
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                                                                                                                                             vngfgrig 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
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                                                                                                                                                                                       Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lodes MJ,
                                                                                                                                                                                                                                             124
                                                                                                                                                                                         Conservative
                                             (first entry)
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                                                                                                                                                                                                                                             AA;
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99US-0370838.
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                                                                                                                                                                                                 88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mohamath R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung cancer; cytostatic; vaccine
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                                                                                                                                                                                               Score 38; Pred. No.
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                                                                                                                                                                                     Mismatches
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1.2;
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                                                                                                                                                                                                         Length 124;
                                                                                                                                                                                                                                                                                                                                                                                 for cancer
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RESULT 13
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Best Local Similarity
Matches 7; Conser
02-APR-1999;
                                          30-MAR-2000; 2000WO-US08560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes lung tumour specific polynucleotides and tumour antigens. 207144 to 207246 and Z08301 to Z08325 represent specifically claimed polynucleotides, and Y29486 to Y29571 represent amino acid sequences from the present invention. The lung tumour specific polynucleotides and polypeptides can be used in pharmaceutical compositions and vaccines to inhibit the development of lung cancer. They can also be used to detect lung cancer in a patient. Probes and antibodies derived from the lung tumour sequences are useful in
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                              Lung tumour protein; lung cancer; cytostatic; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
28-JAN-1998;
28-JAN-1998;
18-MAR-1998;
18-MAR-1998;
23-JUL-1998;
                                                                                                   12-OCT-2000
                                                                                                                                                                                                                                                                                               Human lung tumour-specific antigen encoded by cDNA #58
                                                                                                                                                                                                                                                                                                                                                    05-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             B44447;
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99US-0285323.
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98US-0015029.
98US-0040828.
98US-0040831.
98US-0122191.
98US-0122192.
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87.5%;
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Pred. No. 4.3;
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Best Local S
Matches 7
                                                   04-DEC-1998;
23-DEC-1997;
23-DEC-1997;
23-DEC-1997;
11-JUN-1998;
17-SEP-1998;
                                                                                                                                                                                                                                   Mycobacterium vaccae protein; antigen; T cell activation; Cancer; cancer; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; respiratory system; mycobacterial infection; allergy; tuberculosis; respiratory system; lung cancer; asthma; skin disorder; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-1999;
30-DEC-1999;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              especially lung cancer. Samples of T cells expressing the polypeptides may be used to inhibit the development of cancer. The polypeptides are also useful for detecting and monitoring the progression of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is given in a specification relating to compound for therapy and diagnosis of lung cancer. Polypeptides comprising at least an immunogenic part of a lung tumour protein are disclosed. The polypeptides are useful for inhibiting the development of cancer.
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         Prestidge
                                                                                                                                   23-DEC-1998;
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                                                                                                                                                                              W09932634-A2
                                                                                                                                                                                                    Mycobacterium
                                                                                                                                                                                                                          squamous cell carcinoma; melanoma.
                                                                                                                                                                                                                                                                                                      Amino acid sequence of M. vaccae antigen GV-44.
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                                                                                                                                                                                                                                                                                                                                                  Y14921;
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                              (GENE-) GENESIS RES & DEV CORP LTD.
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DB; C79105.
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7; Conserv
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99US-0476235.
2000US-0518809.
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ω
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                                                  98US-0205426.
97US-0996624.
97US-0997080.
97US-0997362.
98US-0095855.
98US-0156181.
         Skinner MA,
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87
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Pred.
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        Visser ES,
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Query Match
Best Local Similarity
""+"hes 7; Conserv
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Y07036
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Pfreundschuh M
                                                                                                                     22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulatory molecules on cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eszema, allergic contact dermatitis, eszema, allergic contact dermatitis,
                                                                                                                                                                                                                                                                                                     Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides heat-killed Mycobacterium vaccae, or
                                                                                                            11-OCT-1997;
                                                                                                                                                                                               15-JUL-1998;
                                                                                                                                                                                                                       28-JAN-1999
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                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                           Breast cancer associated antigen precursor sequence.
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                                                                                 (LUDW-) LUDWIG INST CANCER RES
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7 vngfgrig 14
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                                                                                                                                                                                                                                                                                             cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 AA;
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97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
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                                             O'Hare M, (
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Pred. No. 9.
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WPI; 1999-132448/11

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The invention relates to a method for diagnosing a disorder characterised CC by expression of a human cancer associated antigen precursor coded for by CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a CC binds to the NAM, an expression product or a fragment that specifically CC binds to the NAM, an expression product or a fragment of an expression CC interaction between the agent and the NAM or the expression product as a CC interaction between the disorder. The products and methods can be used in CC determination of the disorder. The products and methods can be used in CC the diagnosis, monitoring, research, or treatment of conditions CC characterised by the expression of various cancer associated antigens. CC which are cancer associated antigen precursors expressed in human breast CC which are cancer associated antigen precursors expressed in human breast CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
Search completed: June 13, 2001, 14:25:49 Job time: 668 sec
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Best Local Similarity
Matches 7; Conserv
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8 vngfgrig 15
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Pred. No. 12;
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Listing first 45 summaries
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      Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq
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2: pir2:*
3: pir3:*
4: pir4:*
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93.0
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glyceraldehyde-3-p
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-333 <DAV>
A;Rote: the source species is not provided by the authors
A;Note: the source species is not provided by the authors
A;Note: the source species is not provided by the authors
A;Note: the source species is not provided by the authors
A;Tote: Studies of asymmetry in the three-dimensional structure of lobster D-glycera
                                                                                                                                                                           A;Title: Amino-acid sequence of glyceraldehyde 3-phosphate dehydrogenase A;Reference number: A93153; MUID:68098010
A;Accession: A00369
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A;Residues: 45 <HA2>
C;Comment: Cys-149 covalently binds glyceraldehyde-3-phosphate.
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
E;2-32/Region: beta-alpha-beta NAD nucleotide-binding fold
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                                                                                                                                                                                                                                                               R; Davidson, B.E.; Sajgo, M.; Noller, H.F.; Nature 216, 1181-1185, 1967
                                                                                                                                                                                                                                                                                                                        glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - American lobster C;Species: Homarus americanus (American lobster) C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 31-Dec-1996 C;Accession: A00369
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A; Residues: 1-44,'E',46-332 <HAR>
R; Harris, J.I.; Davidson, B.E.; S;
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                                                                                                                                                 A;Molecule type: protein
A;Residues: 1-25 <SOU>
C;Superfamily: 9.1/yceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; hibernation; homotetramer;
                                                                                                                                                                                                                           Biochim. Biophys. Acta 1292, 177-187, 1996
A;Title: Evidence for a posttranslational covalent modification of liver glyceraldehyde-A;Reference number: S62673; MUID:96139342
A;Accession: S62673
                                                                                                                                                                                                                                                                                                                                              glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), hibernating tissue - C:Species: Jaculus orientalis (desert jerboa) C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 19-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Bacillus coagulans (tentative C;Species: Bacillus coagulans C;Date: 05-Jun-1987 #sequence_Crevision 05-Jun-1987 #text_change 31-Mar-2000 C;Accession: A19822; A05100 C;Accession: A19822; A05100 C;Accession: A19822; A05100 C;Crabb, J.W.; Murdock, A.L.; Suzuki, T.; Hamilton, J.W.; McLinden, H.; Amelunxen, R.E. J. Bacteriol. 145, 503-512, 1981 A;Title: Sequence homology in the amino-terminal and active-site regions of thermolabila A;Reference number: A91788; MUID:81117013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A92188; MUID:76069246
A;Contents: annotation; X-ray crystallography, 2.9 angstroms
A;Note: the source species is not provided by the authors
R;Allison, W.S.; Kaplan, N.O.
J. Biol. Chem. 239, 2140-2152, 1964
A;Title: The comparative enzymology of triosephosphate dehydrogenase.
A;Reference number: A44655
A;Contents: annotation; source
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: acetylated amino end; gluconeogenesis; glycolysis; homotetramer; pr.2-31/Region: beta-alpha-beta NAD nucleotide-binding fold
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;148,175/Active site: Cys, His #status experimental
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R;Soukri, A.; Hafid, N.; Valverde, F.; Elkebbaj, M.S.;
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RINGULA, T.; Fukuda, T.; Isobe, T.; Okuyama, T. Biochim. Biophys. Acta 991, 56-61, 1989
A.;Title: Specific purification of 91yceraldehyde-3-phosphate dehydrogenase by hydroph A;Reference number: S03922; MUID:89229261
A;Accession: S03922
A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 1-7;31-34 <KRA>
A;Experimental source: heart muscle
A;Experimental source: heart muscle
A;Note: the authors suggest that this protein differs from the form in liver
A;Note: the last four amino acids of this sequence were determined by carboxypeptidas
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
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J. Biol. Chem. 265, 13308-13313, 1990
A;Title: Glyceraldehyde-3-phosphate dehydrogenase
A;Title: Glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-15 <KOC>
R;Krawczyk, E.; Broda, K.; Sidorowicz, A.; Golebiowska, J.; Siemieniewski,
Comp. Biochem. Physiol. B 85, 811-818, 1986
A;Title: Comparative study of the structure of glyceraldehyde-3-phosphate
A;Reference number: A60790; MUID:87132300
A;Accession: A60790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - bovine (fragments) C; Species: Bos primigenius taurus (cattle) C; Date: 05-Jun-1987 #sequence_revision 30-Sep-1993 #text_change 11-May-2000
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R;Kulbe, K.D.; Jackson, K.W.; Tang, J.
Biochem. Biophys. Commun. 67, 35-42, 1975
A;Title: Structural evidence for a liver-specific glyceraldehyde-3-phosphate dehydrog A;Reference number: A94641; MUID:76087882
A;Accession: A12055
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A;Title: Structural evidence for a liver-specific glyceraldehyde-3-phosphate dehydrog A;Reference number: A94641; MUID:76087882
A;Accession: B12055
A;Molecule type: protein
A;Residues: 1-21 <KUL>
A;Residues: 1-21 <KUL>
A;Residues: 1-21 <KUL>
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R:Fillpek, A.; Gerke, V.; Weber, K.; Kuznicki, J.
Bur. J. Biochem. 195, 795-800, 1991
A;Title: Characterization of the cell-cycle-regulated
A;Reference number: S14090; MUID:91153321
A;Accession: S14160
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 91, 185-191, 1990
Gene 91, 185-191, 1990
A;Title: Glyceraldehyde-3-phosphate dehydrogenase mRNA is
A:Deference number: JT0553; MUID:91007274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1992 #sequence_revision
C:Accession: JT0553; S14160
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A;Reference number: S10221; A
A;Accession: S10221
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A; Residues: 2-20, 'FSCD', 25-26, 'D', 28-64, 'I', 66-70, 'F', 72-77, 'F', 79-80, 'VK', 83-86, 'D', 88
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-333 <SAB>
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Gene 91, 185-191, 1990
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A; Residues: 1-333 <VIN>
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R; Vincent, S.;
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C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1
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Nucleic Acids Res. 18, 3054, 1990
                                                                     Query Match
Best Local
Matches
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A; Nolecule type: mRNA
A; Nolecule type: mRNA
A; Nolecule type: mRNA
A; Residues: 235-304, 'F', 306-333 <LEU>
A; Cross references: GB: M29341; NID: g203141; PIDN: AAA40814.1;
A; Experimental source: brain
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C; Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; CC; Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; CF; 3-33/Region: beta-alpha-beta NAD nucleotide-binding fold
F; 3-33/Region: beta-alpha-beta NAD nucleotide-binding fold
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A: Residues: 144-160 < BAI>
A: Residues: 144-160 < BAI>
A: Experimental source: skeletal muscle
R: Leung, T.K.C.; Hall, C.; Monfries, C.; Lim,
J. Neurochem. 49, 232-238, 1987
A: Title: Trifluoperazine activates and release
A: Reference number: A60208; MUID: 87224934
A: Accession: A60208
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A;Cross references: GB:M11561; NID:9205963; PIDN:AAA41795.1; PID:9205964
R;Vospelnikova, N.D.; Safronova, M.I.; Shuvalova, E.R.; Baratova, L.A.; Kniazev, S.P.
Biochem. J. 199, 757-765, 1981
A;Title: Identification of an arginine residue important for catalytic activity in th
A;Reference number: A90313; MUID:82182080
A;Accession: A17155
A;Mccession: A17155
A;Mcleoule type: protein
A;Residues: 117-119,'N',121-122,'T',124-126,'Z',128,'LF',131-133,'BRZH',138,'SK';294-
A;Residues: 117-119,'N',121-122,'T',124-126,'Z',128,'LF',131-133,'BRZH',138,'SK';294-
R;Baibakov, B.A.; Zheltova, A.O.; Belyanova, L.P.; Baratova, L.A.; Vospelnikova, N.D.
Bioorg, Khim. 3, 826-830, 1977
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Jun-1999
C;Accession: A23013; A22939; A22887; A33280; A17155; JN0401; A60208; B17155
R;Fort, P.; Marty, L.; Piechaczyk, M.; El Sabrouty, S.; Dani, C.; Jeanteur,
Nucleic Acids Res. 13, 1431-1442, 1985
A;Title: Various rat adult tissues express only one major mRNA species from
A;Reference number: A23013; MUID:85215556
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A; Residues: 261-323 < FIE>
A; Cross-references: GB: X00972
A; Cross-references: GB: X00972
R; Maehara, Y; Fujiyoshi, T; Takahashi, K;
Biochem. Biophys. Res. Commun. 131, 800-805,
A; Title: 1.5 KB mRNA abundantly expressed in
A; Reference number: A23280; MUID: 86025533
A; Accession: A23280
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A; Reference number: JN0401
A; Accession: JN0401
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R;Piechaczyk, M.; Blanchard, J.M.; Marty, L.; Dani, C.; Panabieres, F.; El Sabouty, Nucleic Acids Res. 12, 6951-6963, 1984
A;Title: Post-transcriptional regulation of glyceraldehyde-3-phosphate-dehydrogenase A;Reference number: A22887; MUID:85014145
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Nuclelc Acids Res. 13, 2485-2502, 1985
A;Title: Isolation and characterization of
A;Reference number: A93562; MUID:85215629
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A; Residues: 1-80,'AN',83-304,'F',306-333 <TSO>
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A; Residues: 1-333 <FOR>
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A;Cross-references: GB:V00407; GB:J00849; NID:g63402; PIDN:CAA23698.1; PID:g1628381 R;Panableres, F.; Piechaczyk, M.; Rainer, B.; Dani, C.; Fort, P.; Riaad, S.; Marty, L.; Biochem. Biophys. Res. Commun. 118, 767-773, 1984 A;Title: Complete nucleotide sequence of the messenger RNA coding for chicken muscle gly A; Reference number: A32737; MUID:84153854
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A; Residues: 1-293, 'H', 295-333 <STO>
A; Residues: 1-293, 'H', 295-333 <STO>
A; Cross-references: GB:M11213; NID:g211796; PIDN:AAA48774.1; PID:g2117
A; Note: the authors translated the codon CAT for residue 294 as Asp
R; Arnold, H.H.; Domdey, H.; Wiebauer, K.; Datta, K.; Siddiqui, M.A.Q.
J. Biol. Chem. 257, 9872-9877, 1982
A; Title: Cloning, partial sequencing, and expression of glyceraldehyde
A; Reference number: I50231; MUID:8265644
A; Accession: I50231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:K01458; NID:g211800; PIDN:AAA48778.1; PID:g211801 R;Stöne, E.M.; Rothblum, K.N.; Alevy, M.C.; Kuo, T.M.; Schwartz, R.J. Proc. Natl. Acad. Sci. U.S.A. 82, 1628-1632, 1985 A;Title: Complete sequence of the chicken glyceraldehyde-3-phosphate dehydrogenase A;Reference number: A22035; MUID:85166184 A;Accession: A22035
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N;Alternate names: GAP dehydrogenase
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A;Accession: A00368
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                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 'G', 198-276,'E', 278-328,'T', 330-33 <AR2>
A; Residues: 'G', 198-276,'E', 278-328,'T', 330-33 <AR2>
A; Cross-references: EMBL:V00406; NID:g63400; PIDN:CAA23697.1; PID:g63401
C; Genetics:
A; Introns: 8/2; 41/3; 77/3; 107/3; 146/2; 173/3; 224/2; 250/3; 278/3; 311/2
A; Introns: 8/2; 41/3; 77/3; 107/3; 146/2; 173/3; 224/2; 250/3; 278/3; 311/2
C; Superfamily: 91yceraldehyde-3-phosphate dehydrogenase
C; Keywords: 91yceraldehyde-3-phosphate dehydrogenase #status predicted
E; 2-33)/Product: 91yceraldehyde-3-phosphate dehydrogenase #status predicted
E; 3-33/Region: beta-alpha-beta NAD nucleotide-binding fold
E; 3-33/Region: beta-alpha-beta NAD nucleotide-binding
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A; Residues: 1-333 <DUG>
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A; Residues: 1-333 < PAN>
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A; Residues: 'G', 198-276, 'E', 278-333 <ARN>
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A; Residues: 1-333 < IMU>
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Nature 302, 718-721, 1983
A;Title: A new troponin T
A;Reference number: I46471
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A; Residues: 33-79 < PUT>
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c; Date: 31-Dec-1991 #sequence_revision C: Accession: S00152
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N; Contains: uracil DNA glycosylase (EC 3.2.2.), nuclear
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 16:Nov-1995 #sequence_revision 08-Feb-1996 #text_change 11-Jun-1999
C; Accession: JC4309; I46482
R; Applequist, S.E.; Keyna, U.; Calvin, M.R.; Beck-Engeser, G.B.; Raman, C.; Jaeck, H. Gene 163, 325-326, 1995
A. mittle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; F;3-33/Region: beta-alpha-beta NAD nucleotide-binding fold F;150,177/Active site: Cys, His #status predicted
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A;Title: Sequence of the rabbit glyceraldehyde-3-phosphate
A;Reference number: JC4309; MUID:96011658
A;Accession: JC4309
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                                                                                                                                                                                A; Pathway: gluconeogenesis; glycolysis A; Note: tetrameric form; cytosol
                                                                                                                                                                                                                          A; Description: oxidoreductase; reversibly catalyzes the
                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:V00884; NID:g1563; PIDN:CAA24253.1; PID:g929756
                                                                                                                  A;Description: DNA repair; uracil DNA glycosylase for base-excision A;Note: monomeric form; nuclear
                                                                               Superfamily: glyceraldehyde-3-phosphate dehydrogenase 
Keywords: cytosol; DNA repair; gluconeogenesis; glyco
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A; Gene:
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Jun-1999
C;Accession: JN0678; S35726
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F; 2-333/Product:
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A; Title: Evidence for a posttranslational covalent modification of liver glyceraldehyde. A; Reference number: S62673; MUID:96139342
A; Accession: S62674
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A;Title: Occurrance of a differential expression of the glyceraldehyde-3-phosphate dehyde-3-phosphate dehyde-3-p
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Sequence and expression of a glyceraldehyde-3-phosphate dehydrogenase-encoding A;Reference number: JN0678; MUID:93292997 A;Accession: JN0678
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A; Residues: 1-333 <WEI>
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A; Residues: 2-26
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C;Date: 28-May-1997 #sequence_revision 12-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC3370; PC4314; S62674
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A;Accession: PC4314 ·
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A; Residues: 1-333 <SOU1>
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7; Conservative
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A;Cross: recommendation of the 37-kDa protein A;Title: Identification of the 37-kDa protein A;Title: Identificatio
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R;Tso, J.Y.; Sun, X.H.; Kao, T.; Reece, K.S.; Wu, R.
Nucleic Acids Res. 13, 2485-2502, 1985
A;Title: Isolation and characterization of rat and human glyceraldehyde-3-phosphate A;Reference number: A93562; MUID:85215629
A;Accession: B22939
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R;Dani, C.; Piechaczyk, M.; Audigier, Y.; El Sa
Eur. J. Biochem. 145, 299-304, 1984
A;Title: Characterization of the transcription
A;Reference number: IS3309; MUID:85051356
A;Accession: IS3309
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A; Residues: 1-224, D, 226-335 < ARC>
A; Cross-references: GB:X01677; GB:K03121; GB:M17851; GB:X01110; NID:g31644; PIDN:CAA2
R; Hanauer, A.; Mandel, J.L.
EMBO J. 3, 2627-2633, 1984
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N;Contains: uracil DNA glycosylase (EC 3.2.2.-), nuclear
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 08-Dec-1994 #text_change 15-Sep-2000
C;Accession: A31988; A00365; A21939; I53309; B22939; A45924; I55258; A41297;
R;Ercolani, L.; Florence, B.; Denaro, M.; Alexander, M.
J. Biol. Chem. 263, 15335-15341, 1988
A;Title: Isolation and complete sequence of a functional human glyceraldehyde
A;Reference number: A31988; MUID:89008430
     A;Cross-references: GB:J02642; NID:g182862; R;Meyer-Siegler, K.; Mauro, D.J.; Seal, G.;
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Cancer Res. 47, 5616-5619, 1987
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A;Cross-references: GB:M17851; NID:g182860; PIDN:AAA86283.1; PID:g182861
A;Cross-references: GB:M17851; NID:g182860; PIDN:AAA86283.1; PID:g182861
P:Tokunaqa, K.; Nakamura, Y.; Sakata, K.; Fujimori, K.; Ohkubo, M.; Sawa
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A; Residues: 2-335 <TS
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A;Accession: I55258
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A; Residues: 1-335 < TOK>
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A; Residues: 1-335 <ERC>
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A; Residues: 292-310,'V',312-335 <DAN>
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El Sabouty, S.; Cathala, G.; Marty,
PIDN:AAA52496.1; PID:g182863
Wurzer, J.; deRiel, J.K.; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAA52518.1;
                                                                                                                                                                                                                                                                                                                                                    displaying
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                                                                                                                                                                                                                                                                                                                                                    a variable interaction
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          Sirover,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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R;Mercer, W.D.; Winn, S.I.; Watson, H.C.

J. Mol. Biol. 104, 277-283, 1976

A;Tille: Twinning in crystals of human skeletal muscle D-glyceraldehyde-3-phosphate dehy A;Tille: Twinning in crystals of human skeletal muscle D-glyceraldehyde-3-phosphate dehy A;Reference number: A3897; MUID:76265083

A;Contents: annotation; X-ray crystallography, 3.5 angstroms

R;Watson, H.C.; Campbell, J.C.

submitted to the Brookhaven Protein Data Bank, June 1983

A;Reference number: A50598; PDB:3GPD

A;Contents: annotation; X-ray crystallography, 3.5 angstroms, residues 2-8, 'D',10-40, 'H', A;Contents: annotation; X-ray crystallography, 3.5 angstroms, residues 2-8, 'D',244-263, 'E',265-168-189,'S',191-197,'G',199-202,'A',204-205,'L',207-224,'D',226-242,'L',244-263,'E',265-168-189,'S',191-197,'G',199-202,'A',204-205,'L',207-224,'D',226-242,'L',244-263,'E',265-168-189,'S',191-197,'G',199-202,'A',204-205,'L',207-224,'D',226-242,'L',244-263,'E',265-168-189,'S',191-197,'G',199-202,'A',204-205,'L',207-224,'D',226-242,'L',244-263,'E',265-168-189,'S',191-197,'G',199-202,'A',204-205,'L',207-224,'D',226-242,'L',244-263,'E',265-168-189,'S',199-202,'A',204-205,'L',207-224,'D',266-242,'L',244-263,'E',265-260,'D',266-242,'L',244-263,'E',265-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260,'D',266-260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A12103; MUID:76067491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:119249; OMIM:138400
A;Map position: 12p13.31-12p13.1
A;Introns: 10/2; 43/3; 79/2; 109/3; 148/2; 175/3; 313/2
C;Complex: homotetramer; crystallizes as two symmetric dimers in which the partners have C;Complex: monomer
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A; Note: monomeric form; nuclear c; Superfamily: glyceraldehyde; phosphate dehydrogenase C; Superfamily: glyceraldehyde; gluconeogenesis; glycolys c; Keywords: cytosol; DNA repair; gluconeogenesis; glycolys e; 2-335/Product: glyceraldehyde-3-phosphate dehydrogenase p; 2-35/Region: beta-alpha-beta NAD nucleotide-binding fold p; 152/Active site: Cys *status experimental p; 159/Active site: His *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: DNA repair; uracil DNA glycosylase for base-excision in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Function: < NUC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: tetrameric form; cytosol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: oxidoreductase; reversibly catalyzes the oxidative phosphorylation of a; Pathway: gluconeogenesis; glycolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function: <CYT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:GAPD
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A; Residues: 4-15 <SIO>
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; Residues: 2-8, 'D',10-40,'H',42-63,'D',65-69,'D',71,'KA',74-82,'EN',85-91,'TA',94-112,
; Residues: 2-8, 'D',10-40,'H',42-63,'DE',281-283,'D',285-287,'GSN',291-293,'I',295-301,'E'
226-242,'L',244-263,'E',265-278,'DE',281-283,'D',285-287,'GSN',291-293,'I',295-301,'E'
; Sloud, M.; Jespersen, L.
; Mol. Biol. 257, 775-789, 1996
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Residues: 1-335 <MEY>
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VNGFGRIG
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Pred. No. 7.3;
1; Mismatches
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Search completed: June 13, 2001, 14:23:13 Job time: 744 sec